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late G1-69 protein T-cell receptor be T-cell receptor be copper resistance	hypothetical prote phosphoglycerate t	plit profell - ESC Ig heavy chain CRD chilin-binding pro 158K excantigen -	lerredoxin az - Ja terrameric protein transaidolase (EC Ig heavy chain CRD	octamer-Dinding pr gamma subunit of P				/ 7 #text_change 05-Nov-1999 H.	fying rabbit alpha- and beta-ventricu 328491	BJ	AAA31415.1; PID:g165539	<pre>i 2; Length 7; le+05; c indels 0; Gaps 0;</pre>				rucei 6 #tav+ chance 07-Vav-1000		sphoenolpyruvate carboxykinase from T	PMID:7766679			; Length 9; 05; 1; Indels 0; Gaps 6;			s (isolate Beigian CV777) (fragment)
30 12 26.7 9 2 PHOLO8 31 12 26.7 9 2 PTOS62 32 12 26.7 9 2 BTOS62 33 11 24.4 5 2 C41225	11 24.4 5 2 11 24.4 6 2	11 24.4 7 2 2 1 1 24.4 8 8 2 2 1 2 4.4 8 8 2 2 1 2 4.4 8 8 2 2 1 2 4.4 8 8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	11 24.4 9 9 2 2 1 1 2 4.4 4 9 9 2 2 3 5 4.4 4 9 9 9 2 2 5 4.4 4 9 9 9 2 5 4.4 4 9 9 2 5 4.4 4 9 9 2 5 4.4 4 9 9 2 5 4.4 4 9 9 2 5 4.4 4 9 9 2 5 4.4 4 9 9 2 5 4.4 4 8 4.4 4 8 4.4 4 8 4.4 4 8 4.4 4 8 4.4 4 8 4.4 4 8 4.4 4 8 4.4 4	10 22.2 4 2	ALIGNMENTS		rkEVOLT 1 146868 alpha-myosin heavy chain - rabbit (fragment)	Cypertes: Orycoolagus cuniculus (gomestic rabbit) Cybate + Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-N CyAccession: 146868 R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.	Froc. Natl. Acad. Sci. U.S.A. 81, 3644-3648, 1984 A/Title: Characterization of genomic clones speci A/Reference number: 146868, MUID:84221901; PMID:6	Afaccessatus: 1400mg Afattus: preliminary: translated from GB/EMBL/DE Afattus: preliminary: translated from GB/EMBL/DE	A.Residues: 1-7 <fri> A.Cross-references: GB:K01698; NID:g165538; PIDN:</fri>	Query Match Best Local Similarity 50.0%; Pred. No. 2.8e+ Matches 2; Conservative 2; Mismatches	Oy 2 LHED 5	: : qg	RESULT 2 SS5696	phosphoencipyruvate carboxykinase - Trypanosoma brucei Cispecias: Trypanosoma brucei Ciare: 28-fort: 606 #cominance regision 03-Nov.1006 #te	C;Accession: S55696 R:Hunt, M.: Koehler, P.	Biochim. Biophys. Acta 1249, 15-22, 1995 A,Title: Purification and characterization of pho	A; Reference number: S55696; MUID:95284106; PMID:7 A; Accession: S55696	A,Status: preliminary A,Molecule type: protein	A;Residues: 1-9 <hun></hun>	Query Match. 37.8%; Score 17; DB 2; Best Local Similarity 33.3%; Pred. No. 2.8e+05; Matches 2; Conservative 3; Mismatches 1	Qy 1 VLHDDL 6	- Ħ	RESULT 3 P00663 membrane protein - porcine epidemic diarrhea virus
5.1.6 Compugen Ltd.		, Search time 24 Seconds (without alignments) 36.063 Million cell updates/sec				ers: 789					predicted by chance to have a score of the result beand printed.			Description	alpha-myosin heavy phosphoeno.pyruvat membrane protesn hucolin, 75K chain	hypothetical prote ribosomal protein elastase - Pseudom	urine glycopeptide transaldolase (EC	verom protein HR-3 macrophage cytotox	trypsin (EC 3.4.21 T-cell receptor be	biotin A - Citroba T-cell receptor be	T-cell receptor be cerebellar degener	T-cell receptor be acetylcholinestera calsequestrin, fas	1-cell receptor be T-cell receptor be T-cell receptor be	ig gamma chain C r phospharidylethano	il a/b- A - Str e synth
Gencore version 5. Copyright (c) 1993 - 2003 Cc	OM protein - protein search, using sw model	Run on: October 20, 2003, 13:42:21 ; St (wit 36.0	Title: Perfect Score: 45 Sequence: 1 vihddllea 9	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 283308 seqs, 96168682 residues	Total number of hits satisfying chosen parameters	Minimum DB seg length: 0 Maximum DB seg length: 9	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Id	3: pira: 3: pira: 4: pira:	No. is the number of results greater than or equal to the	ved by analysis of the summ	Ouery	Score Match Length DB	18 40.0 7 2 146 17 37.8 9 2 855 16 35.6 7 2 P00 16 35.6 7 2 868	16 35.6 8 2 15 33.3 6 2 14 31.1 7 2	14 31.1 8 2 14 31.1 9 2	14 31.1 9 2 1 14 31.1 9 2	3 13 28.9 9 2	12 26.7 4 2	12 26.7 5 2	12 26.7 7 2 2 26.7 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 12 26.7 7 2 3 12 26.7 7 2	12 26.7 8 2 12 26.7 8 2 12 26.7 8 2	12 26.7 9 12 26.7 9 12 26.7 9

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C;Species: Pseudomonas aeruginosa
C;Date: 13-Mar.2997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C;Accession. 250446
R;Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
FEBS Lett. 299, 291.293, 1992
A;Title: 1dentification of cleavage sites involved in proteclytic processing of Pseudomk
A;Reference number: $20446; MJID:92183956; PMID:1544509
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A,Residues: 1-8 <LOT>
C,Comment: The identity of the glycoprotein from which this peptide is derived is unknowned as also been found (see PIR:XGHUE).
C,Superfamily: unassigned animal peptides
C,Keywords: glycoprotein
F,L/Binding site: carbohydrate (Cys) (covalent) #status experimental
                                                                                                       ribosomal protein MRP-S23, mitochondrial - bovine (fragment)
c;Species: Bos primigenius taurus (cattle)
c;Species: Bos primigenius taurus (cattle)
c;Accession: S76764
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Reference number: S78760
A;Accession: B;Reference Database, July 1999
A;Residues: Le GRABA
A;Reference number: Graften
A;Recidues: Le GRABA
A;Reference number: S78760
A;Recidues: Le GRABA
A;Reference number: S78760
A;Recidues: Le GRABA
A;Reference number: S78760
A;Recidues: Le GRABA
A;Recidues: Licohondrion
F;L-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>
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Biochem. J. 123, 25P, 1971
Biochem. J. 123, 25P, 1971
A)Title: Identification in urine of a low-molecular-weight polar glycopeptide A,Reference number: A03168; XJID:72062338; PMID:5126885
A,Reference number: A03188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urine glycopeptide - human
C;Species: Homo sapiens (man)
C;Date: 2C-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
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Best Local Similarity 50.0
Matches 2, Conservative
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A Molecule type: protein
A Residues: 1-7 <KES>
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C.Species: porcine epidemic diarrhea virus
C.Species: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C.Accession: PQ6663
A.Accession: PQ6663
A.Bridgen, A.; Duarre, M.; Tobler, K.; Laude, H.; Ackermann, M.
C. Gen. Virol. 74, 1795-1804, 1993
A.Aritle: Sequence determination of the nucleocapsid protein gene of the porcine epidemic assible gastroenterits virus.
A.Reference number: JQ2191; MUID:93389433; PMID:8397280
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2003
C;Accession: Pc4131
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-9i, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding y for biosynthesis of heme dl.
A;Reference number: JC4552; MJID:96144254; PXID:8566817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 375, 159-161, 1995
A;Title: Hucclin, a new corticosteroid-binding protein from human plasma with structural
A;Reference number: S68004; MUID:96087107; PMID:7498469
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C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
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A;Cross-references: DDBJ:D50473; NID:g1217594
A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
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A;Residues: 1-7 <BRI>
A;Cross-references: GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:g584083
D;Comment: This virus is coronavirus related to human coronavirus 229E.
C;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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A,Molecule type: protein
A,Residues: 1-7 <50G>
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Coll receptor beta chain V-D-J region (clone 13) - rat (fragment)
C.Species: Ratus norvegicus (Norway rat)
C.Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C.Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C.Date: 09-Oct-1994
R.Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J.Exp. Med. 174, 1467-1476, 1991
A.Title: Analysis of T cell receptor beta chains in Lewis rats with experimental aller A.Mocession: PH0942
A.Molecule type: mRNA
A.Molecule type: manalated the codon TGC for residue 2 as Ala
C.Keywords: T-cell receptor
                                                                                                                                                 trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
(Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
(Species: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_charge 07-May-1999
(Accession: A61328
R.Bricteux-Gregoire, S.; Schyns, R.; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema, Blochim. Biophys. Acta 386, 244-255, 1975
A.Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaen creas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rishiuan, D: Campbell, A. Gene 67, 203-211, 1988
Ajricle: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobac A;Reference number: 140697; MUID:89006280; PMID:2971595
A;Accession: 140697
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4 <RES>
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C;Species: Citrobacter freundii
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: 140697
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A,Residues: 1-8 <BRI>
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
E;1-8/Domain: activation peptide #status experimental <APT>
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50.0%; Pred. No. 2.8e+05;
tive 1; Mismatches 1;
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Sest Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 100.
Matches 3, Conservative
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                                4 VLED
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PH0942
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                                                                                                                                                                                                                                                C)Accession: Al2872

R/Sun, S.C.; Joris, L.; Tsolas, O.
Arch. Biochem. Biophys. 178, 69-78, 1977

A)Title: Purification and crystallization of transaldolase isozyme I and evidence for di
A)Reference number: Al2872; MJID:77110646; PMID:556924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              St
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Exp. Hematol. 19, 704-709, 1991
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin A;Reference number: A60427; MUID:91372335; PMID:1909970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-9 <JON>
A,Note: the sequence from the text on page 706 is inconsistent with that from page 708
C,Keywords: cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Verong protein HR-3 - oriental hornet (fragment)
C.Species: Vespa crientalis (criental hornet)
C.Species: Vespa crientalis (criental hornet)
C.Baccession: S10926
R.Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A.Title: Low-molecular-weight peptides of venom of the giant hornet Vespa crientalis. A.Reference number: S16926
A.Rocession: S16926
A.Residues: 1-9 - TUI>
C.Keywords: venom
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                                                                                                                                                                               ransaldolase (EC 2.2.1.2) I - yeast (Pichia jadinii) (fragment)
Species: Pichia jadinii, Candida utilis
Date: 05-Cun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
C;Accession: A60427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.1%; Score 14; DB 2; Length 9; 33.3%; Pred. No. 2.8e+05; tive 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.1%; Score 14; DB 2; Length 9; 28.6%; Pred. No. 2.8e+05;
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Best Local Similarity 33.3
Matches 2; Conservative
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A;Residues: 1-9 <SUN>
C;Reywords: transferase
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Best Local Similarity
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A60427
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Query Match
26.7%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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Profession: 197
Profession: Profession: V-D-J region (120-2K) - mouse (fragment)
Cispecies: was was caused the consequence revision of the consequence of the c

A,Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H C;Keywords: T-cell receptor

Cuery Match 26.7%; Score 12; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels

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34 9 20.0 8 I FUSS FUSSO P81010 fusa 35 9 20.0 9 I PAR4 CALVO P62678 chlar 36 9 1 IPAB PAPA P19343 papis 38 9 20.0 9 I PPAR PAPA P82992 rhode 39 20.0 9 1 PPH1 LYCES P83380 lycol 40 9 20.0 9 1 JAME HOWA P81931 homo 41 8 17.8 3 1 JAME HOMAN P01157 homo 42 8 17.8 4 1 DCML PSECH P01157 homo 43 8 17.8 4 1 DCML PSECH P19916 pseu 44 8 17.8 5 1 308 CITPR P12997 citr 45 8 17.8 6 1 ACPH_RABIT P25154 crycic	ALIGNMENTS	5 6	DI 28-FEB-2003 (Rel. 41, Lest sequence update) DT 28-FEB-2003 (Rel. 41, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DE FNRFamide-like neuropeptide FLPB (VSHNNFLRF-amide). CS Macrobrachium rosenbergii (Giant fresh water prawn). CC Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;		11) SIJU SEUERICE, AND MASS SPECTROMETRY. TISSUE-EYESTAIK; MEDLINE-21107394; Pubmed-:1179812;	Sithigorngul P., Saraithongkum W., Longyant S., Panchan N., Sithigorngul W., Petsom A., "Three more novel FMRFamide-like neurobebtide sequences from	eyestalk of the giant freshwater prawn Macrobrachium ros Peptides 22:197(2001) mass specime-197(2001)	CC -:- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) CC FAMILY. DR GO: 0007218; P:neuropeptide signaling pathway; IDA.	Neuropeptide, Amidation. MOD_RES 9 9 AMIDATION. SEGUENCE 9 AA, 1133 MW, 845A0729C44441F5 CRC	Query Match 35.6%; Score 16; DB 1; Length 9; Best Local Similarity 42.9%; Pred. No. 1.3e+05; Matches 3; Conservative 2; Mismatches 2; Indels 0; G	Qy : VLHDDL: 7 :: :: Ob : VSHNNP: 7	:: i	AC P3614; DT 01-JUN-1994 (Rel. 29, Created) DT 01-JUN-1994 (Rel. 29, Last sequence update) DT 01-FEB-1995 (Rel. 31, Last annotation update) DE TrpBA operon transcriptional activator (Fragment).	utida. eobacteria; Gammaproteo eae; Pseudomonas. 3;	., ., .,
Copyright in - protein search, October 20, SEQ1A	Sequence: 1 vlhddllea 9 Scoring table: BLOSUM62 Gapop 10.C, Gapext 0.5	Searched: 127863 segs, 47026705 residues Total number of hits satisfying chosen parameters: 251	Minimum DB seq length: 0 Maximum DB seq length: 9 Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	Database : SwissProt_41:•	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SURVARIES	ery tch Length DB	1 16 35.6 9 1 FAR8 MACRS P83281 2 14 31.1 6 1 TRP1 FSEPU P56414 3 14 31.1 8 1 GLUR HJMAN P02729	14 31.1 9 1 TALI_PICUA P17446 12 26.7 5 1 BICA_CITER P13071 12 26.7 6 1 TMOF_SARBU P41495	12 26.7 7 1 NEVI SARSU 28841 12 26.7 9 1 RE42_LITRU P82.492 12 26.7 9 1 RE42_LITRU P82.075 12 26.7 9 1 UF02_MOUSE P58645	12 24.4 7 1 FARZ ASCISJ 11 24.4 9 1 FTSP BOXNG PROCOS 11 24.4 9 1 FTSP BOXNG PROCOS 10 22.2 7 1 ALL7 CYDPC PROCES	10 22.2 7 1 HY7 FIG POLISS 10 22.2 7 1 PPH7 LYCES P83379 8 10 22.2 7 1 UNOG PINPS P81675 10 22.2 8 1 ANG2 BOTUA Q10582	10 22.2 8 1 P.P. SKANA P9107 10 22.2 8 1 UF06 MOUSE P38644 10 22.2 9 1 F18B ERYPA P15346 4 10 22.2 9 1 LMIP LOCMI P31799	0 22.2 9 1 ULAH_HUMAN P11534 9 20.0 5 1 E103_LITRU P82039 9 20.0 5 1 E104_LITRU P82109 9 20.0 5 1 TRM3_ECOLI P13973 9 20.0 6 1 ASP2_LACSN P82655 9 20.0 7 1 ALIZ CARNA P81805	1 9 20.0 7 1 FARI_HELTI P41871 helisoma 2 9 20.0 7 1 FARB_CALVO P41866 callipho: 3 9 20.0 8 1 FAR8_CALVO P41863 callipho:

P81010 fusarium so	P62678 chlamydomon	P41859 calliphora			P83380 lycopersico	P31931 homo sapien	P01157 homo sapien		P19916 pseudomonas	P12997 citrobacter	P25154 orygtolagus
FUSS_FUSSO	ALC CHLRE	FAR4 CALVO	FI3B PAPHA	I PYR RHOVI	PPH1_LYCES	ULAE HUMAN	GRWM HUMAN	THYL PIG	DCML_PSECH	SIOB_CITFR	ACPH_RABIT
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3.4	35	36	3.7	38	39	40	۲. ۲.	42	43	44	4.5

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                :-like neuropeptide sequences from the water prawn Macrobrachium rosenbergii.";
                                                                                                                                                                                                                                                                                                                                                 133.8; METHCD=MALDI.
THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                              .179812;
jkum W., Longyant S., Panchan N.,
                                               t sequence update)
t annotation update)
de FLPB (VSHNNFLRF-amide).
(Giant fresh water prawn).
opoda; Crustacea; Malacostraca;
Decapoda; Pleocyemata; Caridea;
ae; Macrobrachium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; Length 9;
Pred, No. 1.3e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    ide signaling pathway; IDA.
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845A0729C44441F5 CRC64;
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annotation update)
al activator (Fragment).
9 AA.
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PRT;
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Arch. Blocker. Blophys. 178:69-78(1977).

-!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF METABLOLISES IN IMPORTANT FOR THE BALANCE OF METABLITES IN THE PENTOSPHATE PATHWAY.

-!- CATALTIC ACTIVITY: Seacheptulose 7-phosphate + D-fructose 6-phosphate.

3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.

-!- PATHWAY: Pentose phosphate pathway; nonoxidative part.

-!- STMILARITY: BELONGS TC THE TRANSALDOLASE FAMILY. SUBFAMILY 1.

FIR, A12872; A22872.

InterPro; IPR001585; Transaldolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Transcriptional regulation and gene arrangement of Escherichia coli, Cirobaccer freundii and Salmonella typhimurium biotin operons."; Gene 67:203-211(1988).
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01-0AN-1990 (Rel. 13, Last sequence update)
01-0AN-1990 (Rel. 40, Last annotation update)
Adenosylmethionup. 40, Last annotation update aminotransferase
EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                          Bukarycta, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes,
Saccharomycetales; Saccharomycetaceae; Pichia.
NCBI_TaxID=4903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cxononandate = S-adenosyl-4-methylthio-2-cxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sun S.C., Joris L., Tsolas O., Purification of transaldolase isozyme I Purification of crystallization of transaldolase isozyme I evidence for different genetic origin of isozymes I and III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.1%; Score 14; DB 1; Length 9; 33.3%; Pred. No. 1.38+05; cive 2; Mismatches 2; Indels
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                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Examaldolase I (EC 2.2.1.2) (Fragment)
Pichia jadinii (Yeast) (Candida utilis).
                                                                                        9 A.
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PROSITE; PS01054; TRANSALDOLASE 1; PARTIAL.
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-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89006280; Pubmed=2971595;
Shiuan D., Campbell A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=77110646; PubMed=556924;
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Matches 2, Conservative
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                     TALL PICUA
ID TALL PICA
AC P17440;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
BIOA_CITFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPPORTANT MARKAN MARKAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EXBL cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
O
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"Identification in urine of a low-molecular-weight highly polar
glycopeptide containing cysteinyl-galactose.";
Blochem, J. 123:259-259(27);
-:- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS FEPTIDE
IS DERIVED IS JUNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED. AN EXTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A
SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
PIR; A03188; XGHUBU.

GO; GO:COOS576; C:extracellular; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                  Biochimie 71:521-531(1989).

-:- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOCEDINGENCE PHOSPHATE), TRP1 BINDS UPSTREAM OF THE TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

-:- SIMILARITY: BELCNGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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   Eberly L., Crawford I.P.; "DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000847; HTH LySR.
PROSITE; PS00044; HTH LYSR FAMILY; PARTIAL.
Tryptophan biosynthesis; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.1%; Score 14; DB 1; Length 8; 100.0%; Pred. No. 1.3e+05; tive C; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 1 S-LINKED (GAL. .). 8 AA; 855 MW; C2D87AA:F581EBLE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA; 683 MW; 77672AAIEDD6F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.1%; Score 14; DB 1; Le
100.0%; Pred. No. 1.3e+05;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=72062338; PubMed=5126885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X13299; CAA31660.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Crawford I.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Past 2; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Urine glycopeptide.
                                                                                                                                                                                                                                                                                 REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 HD 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 HD 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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P02729:
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SEQUENCE
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GLUR HUMAN RESULT 3

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Neosulfakinin-I (NEB-SK-I).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Sukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endoprerygota, Diptera, Brachycera, Muscomorpha, Oestroidea,
Sarcophagidae, Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE.

TISSUE=Fibroblast;

WEDLIKE=9500907; PubMed=7523108;

WEDLIKE=9500907; PubMed=7523108;

Merick B.A., Patterson R.M., Wichter I.L., He C., Seiktrk J.K.;

Merick B.A., Patterson R.M., Wichter I.L., He C., Seiktrk J.K.;

Merick B.A., Patterson R.M., Wichter I.L., He C., Seiktrk J.K.;

Merick B.A., Patterson R.M., Wichter I.L., He C., Seiktrk J.K.;

Merick B.A., Patterson R.M., Wichter I.L., He C., Seiktrk J.K.;

Merick B.A., Patterson R.M., Miller B.A., Patter 
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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0
                          01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last amodation update)
Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.7%; Score 12; DB 1; Length 9; 100.0%; Pred. No. 1.3e+05; Attive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7;
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9 AA; 1187 MW; 8BOAO691E86BSAAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULFATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
26.7%; Score 12; DB 1; I
Best Local Similarity 33.3%; Pred. No. 1.3e+05;
Matches 1; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 33, Last annotation update)
Neosulfakinin-I (NBB-SK-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
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MOD RES 4 4 4 SULFAT MOD_RES 9 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93083101; PubMed=1360367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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ID RE42_LITRU
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SEQUENCE.
                                                                                                                                                                                                                                                                              SECUENCE
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Oestroidea,
Sarcophagidae, Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequencing and characterization of trypsin modulating obstatic
factor (TMOF) from the cvaries of the grey fleshfly, Neobellieria
(Sarcopiaga) bullata.";
Regul. Pept. 50:61-72(1994).
-! FUNCTION: HAS AN OGSTATIC ACTIVITY. INHIBITS TRYPSIN BLOSYNTHESIS
-! FUNCTION: HAS AN OGSTATIC ACTIVITY REDUCES THE VITELOGEN:N
IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELOGEN:N
CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OCCYTE
-:- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Ovary;
BEDLINE=9421:930; PubXed=8159807;
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-PEB-1996 (Rel. 33, Last annotation update)
Trypsin-modulating oostatic factor (TWOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.7%; Score 12; DB 1; Length 6; 100.0%; Pred. No. 1.3e+05; Astive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.7%; Score 12; DB 1; Length 5; 100.0%; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR005814; Aminotrans 3.
PROSITE; PS00600; AA TRANSFER_CLASS_3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
Pyridoxal phosphate.
NON TER
SEQÜENCE 5 AA; 582 MW; 6AAABIBIA6F00000 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AA; 695 MW; 61E72451B7642000 CRC64;
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F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                         EMBL; M21922; -; NOT ANNOTATED_CDS.
PIR; 140697; 140697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND SYNTHESIS.
                                aminotransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7385;
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ID UF03_MOUSE
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TMOF_SARBU ID TMOF_S

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Gaps

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Gaps

Hormone

Matches

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PRT;
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   20.0%;
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Matches 2, Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                   STANDARE;
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Best Local Similarity
Matches 1; Conserv
                                                                                                            2 LHDDL 6
                                                                                                                                                    : .::
MEDEI 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAR2_ASCSU
P31890;
                                                                                                                                                                                                                                                                                                                                                   HUYFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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FAR2_ASCSU
                                                                                                                                                                                                                                                                                  RESULT 11
JEA2_HUYAN
                                                                                                                                                                                                                                                                                                                                                       JH42
                                                                                                                                                                                                                                                                                                                                                           SOUTH TANK SAN SOUTH TO SEE THE SOUTH THE SOUT
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-:- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skin secretion;
Steinborner S.T., Wannitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wannitz P.A., Waugh R.J., Bowie J.H., Gao C.,
"Tyler M.J., Wallace J.C.,
"The structure of new peptides from the Australin red tree frog
'Liccria rubella', The skin peptide profile as a probe for the study
Clicoria rubella', The skin peptide profile as a probe for the study
Aust. J. Chem. 49:955-963 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skin secretion, Tyler M.J., Wallace J.C.; Wabhitz P.A., Sowie J.H., Tyler M.J., Wallace J.C.; Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCSI_TaxID=10090;
                                                                                                                                             Rubellidin 4.2/4.3.
Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aust. J. Chem. 52:639-645(1999).
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01-OCT-1994 (Rel. 30, Last sequence update)
01-CT-1994 (Rel. 31, Last annotation update)
Unknown protein from 20-page of fibroblasts (P32) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.7%; Score 12; DB 1; Length 9; 66.7%; Pred, No. 1.3e+05; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- MASS SPECTROMETRY: WM=883; METHOD=FAB.

Amphibian defense pepide; Amidation.

MOD RES
SEQÜENCE 9 AA; 884 WW; 2C2D77205AA72728 CRC64;
                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA
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SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND MASS SPECTROMETRY.
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Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                          NCB1_TaxID=104895;
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              P82093;
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P38640;
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UF02_MOUSE
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Dp
              SEET RESCOULD CONTRACT TO THE RESCOULD CONTRAC
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DB 1; Length 9;

26.7%; Score 12;

Query Match

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MEDLINE=93324431; PubMed=8332542;
Cowden C., Stretton A.O.W.;
"APE, an Ascaris neuropeptide: isolation, sequence, and bloactivity.";
Peptides 14:423-430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present in the
Rhabditida).";
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                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoldea;
Ascarididae; Ascaris.
NCE_TaxiD=6253, 6233;
                                                                                                                                                                                                                                                                                                                                                                                                                      Electrophoresis 15:1459-1465(1994).
-!- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.0, ITS WM IS: 55.3 kDa.
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95203287; PubMed=7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
1994."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
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0
                                                                                                                                                                      P40929;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Unknown protein From 2D-page of heart (Spot 5603) (Pragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUD-1993 (Rel. 26, Created)
01-JUD-1993 (Rel. 26, Last sequence update)
01-FDB-1996 (Rel. 13, Last ammotation update)
FWRFamide-like neuropeptide AP2.
Ascaris squm (Pig roundworm) (Ascaris lumbricoides), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
Pred. No. 1.3e+05;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%; Score 12; DB 1; Length 9; 100.0%; Pred. No. 1.3e+05;
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SEQUENCE 9 AA; 1104 MW; 8874BIBB5B01B2CA CRC64;
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                                                                                                                                                          9 AA.
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MEDLINE=75145197; PubMed=1092268;
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3 IHCNTL 9
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NCBI_TaxID=82600;
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P82158;
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NON TER
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ALL7_CYDPO
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Neoptera: Endopterygota: Lepidoptera: Glossata: Ditrysia: Bombycoidea:
NoSI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a prothoracicostatic peptide in the larval brain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transaldolase III (EC 2.0.1.2) (Fragment).
Pichia jadinii (Yeas) (Candida utilis).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTICE)
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Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
Kataoka H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11; DB 1; Length 9;
Pred. No. 1.3e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                     24.4%; Score 11; DB 1; Length 7; 50.0%; Pred. No. 1.3e+05; ive 1; Mismatches 1; Indels

        MOD_RES
        9
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        9
        AMIDATION.

        SEQUENCE
        9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;

                                                                                                                              SEQÜENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTSP_BOWNO STANDARD; PRT; 9 AA. P82062.
P82062.
P82062.
P82062.
P82062.201 (Rel. 40, Last sequence update)
P8-F28-2003 (Rel. 41, Last annotation update)
P8-PRD-ADARACTOSTATIC pepilde (Bcm-PTSP).
P8-PRD-YX mort. (Silk moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA.
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: BARLY FIFTH INSTAR.
                                                                                                    AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the silkworm, Bcmbyx mori.";
J. Biol. Chem. 274:31169-31173(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
STRAIN=C145 X N140; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.4%;
                                                                                                                                                        Query Match
Best Local Similarity 50.0.
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                                   FAMILY.
Neuropeptide; Amidation.
MOD RES 7 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hormone, Amidation.
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                    2 HEYL 5
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TAL3_PICJA
ID TAL3_PICJA
AC P17441;
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TSOLAR O., Sun S.C.;

"Isolation of a peptide containing a histidinyl-cysteinyl sequence
"Isolation of Isolation of Itanian Isolation Isol
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MEDLINE=98054539; PubMed=9392829;

MEDLINE=98054539; PubMed=9392829;

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davey M., East P.D., Thorpe A.;
Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997);

Peptides 18:1301-1309(1997);

Peptides 18:1301-1309(1997)

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Eukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neopiera, Endopterygota, Lepidoptera, Glossata, Ditrysia;
Tortricoidea, Tortricidae, Olethreutinae, Cydia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; Score 11; DB 1; Length 9; 33.3%; Fred. No. 1.3e+05; tive 2; Mismatches 2; Indels
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30-MAY-2200 (Rel. 39, Last sequence update)
30-MAY-2200 (Rel. 39, Last annotation update)
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051594 escherichia 090464 appergillus 01588 hamo sapian 037854 bacteriopha 08222 dayctobacill 049223 qlycine max 08kpx4 microcystis 01589 homo sapian 08mun6 heliconius 09065 taxius 090400 masoala mad 09147 mesoricetu 09140 masoala mad 09140 masoala mad 09140 masoala mad 09569 quilus gailus gallus gallu

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saccharomyc homo sapien homo sapien synechococc

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SEQUENCE OF 1-5 FROM N.A.
MEDLINE=83195078; PubMed=6302686;
HOOVEY T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
Wild J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEÇJENCE FRCM N.A. SEÇJENCE FRCM N.A. SECHACHMAN H.K.; Pauza C.D., Karels M.C., Navre M., Schachman H.K.; Genze encoding Escherichia coll aspartate transcarbamoylase: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria: Proteobacteria, Gammaproteobacteria; Enterobacteriales,
Enterobacteriaceae; Escherichia.
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Pred. No. 8.3e+05;
2; Mismatches 1; Indels
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Last sequence update)
regulatory chain (Fragment).
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EMBJ, J01670, AAA24475.1; -.
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08MUN6
09N6MS
08WNS1
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Q16605
Q9BQT4
Q61723
Q92766
Q8AYL5
Q8AUM7
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Q8G1Z6
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Q15897
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50.0%;
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Best Local Similarity 50.0v
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01-NCV-1996 (TrEMBLrel.
01-NCV-1998 (TrEMBLrel.
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pyr8-pyrI
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                                                                                         October 20, 2003, 13:41:46 ; Search time 59 Seconds (without alignments) 39.364 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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ventricular myosin heavy chains.";
Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
EXBL; K01698; AAA31415.1; -.
NON TER 1 1.15.1; SEQÜENCE 7 AA; 916 MW; 6BIBIAAIB69326B0 CRC64;
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Murphy W.J., Thomerson J.E., Collies G.E.;
"Phylogeny of the Neotropical Killifish family Rivulidae
"Cyptinodontiformes, Aplochalloidel) inferred from mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyptinodontiformes; Aplocheilidae; Rivulinae; Gnatholeolas.
ONDI_TaxID=135316;
                                                                                                                                                                                                                  Alpha-myosin heavy chain (Fragment).

Oryctolagus cuniculus (Rabbit).

Oryctolagus cuniculus (Rabbit).

Mammalla; Exineria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=8421901; PubMed=6128491;
Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.
Rabinowitz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.6%; Score 16; DB 8; Length 7; 42.9%; Pred. No. 8.3e+05; tive 2; Mismatches 2; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Phylogenet. Evol. 13:289-301(1999)
EMBL; AF002591; AAD01074.1; -.
                                                                                                                PRT;
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CCI.
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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3 HDNKLQ
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3 MHDE 6
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NON TER
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                                                                                                                                                                                                                                                                                                         Hogan D.A., Du P., Stevenson T.I., Whitton M., Kliby G.W., Rogers J., VanSogelen R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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STRAIN-cv. C123;
Ching A.S., Culdwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
Abregante M., Rafalski J.A.;
SNP frequency, hazplotype structure and linkage disequilibrium in
elite maize inbred lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoilophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0, Indels
                                                                                                                                                   35.6%; Score 16; DB 2; Length 9; 40.0%; Pred. No. 8.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2000) to the SWISS-PROT data bank.
-:- NASS SPECTROMETRY: WW=22592.C4; METHOD=ELECTROSPRAY.
NON_TER 1 1 1 1 NON_TER 2 5 SEQUENCE 9 AA; 1069 WW; 2A771042CB1AB2D7 CRC64:
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Last sequence update)
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P82568
P82568:
01-0CT-2000 (TEMBLEE) 15, Created)
01-0CT-2000 (TEMBLEE) 15, Last sequence
01-0CT-2000 (TEMBLEE) 15, Last annotati
Unknown protein from 2D-page (Fragment)
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01-007-2002 (TrEMBLrel. 22, Last sequen
01-007-2002 (TrEMBLrel. 22, Last annota
Beta-expansin-like protein (Fragment).
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                                                                                                                                                                                                                                                                          AND MASS SPECTROMETRY.
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Matches 2, Conservative
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Gaps

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Sidnu M.S., Heir B., Sorum H., Holok A.L.;
"Genetic linkage between quaternary ammonium compound and beta-lactam
resistance in Staphylococci isolated from food.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYC28779; AAX38453.1; -.
                                                                                      SEQUENCE FROM N.A.

MEDLINES-95255652; Pubmed=7737502;

Asturias J.A., Diaz E., Timmis K.N.;

Asturias J.A. Diaz E., Timmis K.N.;

Svointionary relationship of the biphenyl dioxygenase of the grampositive bacterium Rhodococcus globerulus P6 to multicomponent gramnegative bacteria.";

Gene 156:11-1811995).

EMBL; X80041; CAA56350.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macroscelides proboscideus (Short-eared elephant shrew).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Macroscelidea, Macroscelididae, Macroscelides.
      Bactería, Actinobactería, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                             31.1%; Score 14; DB 2; Length 8; 33.3%; Pred. No. 8.3e+05; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.1%; Score 14; DB 2; Length 8; 50.0%; Pred. No. 8.3e+65; tive 2; Mismatches 0; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
04-JUN-zesponsive element moderator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                              NON TER 8 6
SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Staphylococcus
NCBI_TaxID=1282;
                  Corynebacterineae; Nocardiaceae; Rhodococcus, NCSI_TaxID=33008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis.
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Best Local Similarity 50.v.
2, Conservative
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Best Local Similarity 33.3
Matches 2; Conservative
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L2DEVV 8
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SEQUENCE
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Q93SR0;
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Q9BFA7
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0935R0
    STARRED SOCO
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Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A.; Baldini A., Lindsay E.A., Zhao Z.-Y.,
                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation of additional bacteriophages with genomes of segmented
                                                                                                                                                                                                                                                                                       Caskey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL; L32079; AAA73890.1;
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BDLINE=99383412; PubMed=10419946;
Mindtch D., Qiao X., Qiao Č., Onodera S., Romantschuk M.,
Hoogstraten D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 4; Length 8; Pred. No. 8.3e+35; 1; Mismatches 3; Indels
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40.0%; Pred. No. 8.3e+05;
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Biphenyl dioxygenase (Fragment).
C1-NOV-1996 (TrEMBirel, 01, Created)
C1-NOV-1996 (TrEMBirel, 01, Last sequence update)
C1-DEC-2001 (TrEMBirel, 19, Last annotation update)
(Clone XP7PBilA) (Fragment).
Homo sapiens (Human).
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Last sequence update)
Last annotation update)
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Viruses, dsRNA viruses, Cystoviridae, Cystovirus.
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EMBL; AF125675; AAD22555.1;
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Best Local Similarity 94...
"wes 3; Conservative
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les 2; Conservative
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                         NCBI_TaxID=9606;
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Eukaryota, Mětazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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MEDLINE=84115080; PubMed=6119754;
Lerner T.L., Hanafusa H.;
Lerner T.L., Hanafusa H.;
Low sequence of the Bryan high-titer strain of Rous sarcoma virus:
Extent of env deletion and possible genealogical relationship with
other viral strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taxemura M., Yamauchi K., Yamatodani A., "Structural analysis of histamine N-methyltransferase gene."; Methods Find Exp. Clin. Pharmacol. 17:1-4 (1995).
Transferase; Methyltransferase.
                                                                             Query Match. 31.1%; Score 14; 3B 11; Length 9; Sest Local Similarity 75.0%; Pred. No. 8.3e+05; Matches 3; Conservative 0; Mismatches 1; Indels
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31.1%; Score 14; DB 15; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.38+35;
Matches 3; Conservative 1; Mismatches 2; Indels
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SQ SEQÜENCE 9 AA, 994 MW, 342161AB172EBAB7 CRC64;
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EMBL; K03265; AAA42557.1; -.
SEQUENCE 9 AA, 949 MM; 94AA144DDDD731AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley, TISSUE=Liver,
MEDLINE=96342418; PubMed=8750786;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
SEQUENCE FROM N.A.

MEDLINE=21082082; PubMed=11214319;

Murphy W.C.; Ezirik E., Johnson W.E., Zhang Y.P., Ryder C.A.,
O'Brien S.J.;
"Molecular phylogenetics and the origins of placental mammals.";
"Molecular phylogenetics and the origins of placental mammals.";
Nature 409:614-6181201).

BEL, AY011636, AAG4751.1; -.
NOW TER 1
SEQÜENCE 8 AA, 940 MW; DFIDD33AB5AB572A CRC64;
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Dopico B., Jimerez T., Labrador E.;
"CDNa clones expressed in etiolated Cicer arietinum epicotyls.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ299069; CAC10216.1;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-type lectin DCL1 (Fragment).
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GenCore version 5.1.6
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ALIGNMENTS

The Admy 1375 standard, Protein; Admy 1375, 13-May-1999 (first entry) Admy 1375, 14-1 H-allele sequence. Intron; minor histocompatibit allele, R allele, polymorpone marrow transplant; sevenome activition disease; shown sapiens. MOP905313-A2. M	atandard. Proteir. 9 AA								ibility antigen HA-1; typing allele;	Hallele, Rallele, polymorphic nucleotide, HA-1 typing,	bone marrow transplant; severe aplastic anaemia; leukaemia;									28.		25.	03.						
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and

Typing minor histocompatibility antigen HA-1 - by amplifying identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection of genetic aberrances

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The present sequence represents part of the minor histocompatibility antigen HA-1 H-allele. The specification describes methods for typing alleles (preferably the H and R alleles) of the minor histocompatibility antigen HA-1 in a sample, which comprise detecting polymorphic nucleotides in the cDNA or genomic nucleic acids of the alleles. The methods can be used for HA-1 typing for bone marrow transplants, severe applastic anaemia, leukaemia and immune deficiency diseases, as well as detection of genetic aberrances. The probes and primers of the invention can be used to screen for the HA-1 alleles. The HA-1 peptides can be used anti-idiotypic B cells and/or T cells and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents a new peptide (P1) constituting a T-cell
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                                                                                       Claim 18; Fig 5; 59pp; English
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1 VLHDJLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                          9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4AM99196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents part of the minor histocompatibility antigen KA-1 R-allele. The specification describes methods for typing antigen KA-1 R-allele. The specification describes methods for typing antigen KA-1 in a sand, which comprise detecting polymorphic nucleotides in the CBNA or genomic nucleic acids of the alleles. The methods can be used for HA-1 typing for bone marrow transplants, severe applastic ansemia, lewaemia and immune deficiency diseases, as well as detection of genetic aberrances. The probes and primers of the invention can be used to screen for the HA-1 alleles. The HA-1 peptides can be used anti-idiotypic B cells and/or T cells and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                       Intron, minor histocompatibility antigen HA-1; typing allele; H allele, R allele, polymorphic nucleotide, HA-1 typing; bone marrow transplant; severe aplastic anaemia; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Typing minor histocompatibility antigen HA-1 - by amplifying identifying EA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection of genetic aberrances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.2%; Score 37; DB 20; Length 9; 88.9%; Pred. No. 9.3e+05; Live 0; Mismatches 1; Indels
                                                        0; Indels
                         100.0%; Score 45; DB 20;
100.0%; Pred. No. 9.3e+05;
                                                        0; Kismatches
                                                                                                                                                                                        AAW97374 standard; Protein; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Fig 5; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                    immune deficiency disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-EP04928
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYLE-) RICKSUNIV LEIDEN
                                                                                                                                                                                                                                                                          HA-1 R-allele sequence
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                                                                                    1 VLHDDLLEA 9
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                                                                                                      1 VLHDDLLEA
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Matches 8; Conserv
                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-1997;
                                                                                                                                                                                                                                               13-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-1999.
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                                                                                                                                                                                                                  AAW97374;
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 Sequence
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                                                        Watches
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Gaps

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RESULT 4

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(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                        9 AA;
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                                                                                                           Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-YAY-1959
                                                                     23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Home sapiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1998;
           WC9905173-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WC9905174-A1
                              04-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                         Sectional
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
AAW99195
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                                                                                                                                                                                                                                                                                                                                 The present sequence represents a new peptide (Pl) constituting a T-cell epitope obtainable from the minor histocompatibility antigen (M-1. The optide is immunogenic and can be used as part of a vaccine. It is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leuxaemia, and immune deficiency diseases.
                                                                            Minor histocompatibility antigen; HA-i; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anaemia; immune deficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell epitope; minor histocompatibility antigen HA-1; vaccine; transplant rejection; Graft-versus-Host Disease; autoimmune disease; neoplastic haematopoletic cell.
                                                                                                                                                                                                                                                                         A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell epitope from the minor histocompatibility antigen HA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 20; Length y;
Pred. No. 9.3e+05;
Pred. non+ohes 1; Indels
                                                          Minor histocompatibility antigen HA-1 T-cell epitope #3
                                                                                                                                                                                                                                     DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key Location/Qualifiers
Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "His or Arg"
                                                                                                                                                                                                                                                                                                                Disclosure, Page 15; 47pp; English.
                                                                                                                                                                                                                                      Hunt
AAW99197 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97572 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%;
                                                                                                                                                                                                                                     Goulmy EAJY,
                                                                                                                                                                             58WO-NL30425
                                                                                                                                                                                                97EP-0202303
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                 (UYLE-) RICKSUNIV LEIDEN
                                                                                                                                                                                                                                                        WPI; 1999-153312/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VERDDLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VLHDCLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                        9 24
                                                                                                                                                                                                                                     Engelhard VH,
                                                                                                                                                                                                23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                     Homo sapiens
                                                                                                                                      W09905174-A1
                                                                                                                                                                            23-JUL-1998;
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                                                                                                                                                         04-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW97572;
                   AAW99197;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present sequence represents an immunogenic peptide constituting a 1-cell epitope, obtainable from the minor histocompatibility antigen HA-1. The peptide can be used in vaccines or pharmaceutical formulations as medicines to induce tolerance for transplants so as to prevent rejection and/or Graft-versus-Host Disease, or to treat autoimmune diseases. Neoplastic haematopoletic cells presenting the peptides, in an HLA class I context, can be eliminated after specific recognition of the peptides. The peptides can also be used to raise antibodies, I-cell receptor, B- and I-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anacmia; immune deficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                          Immunogenic peptide from minor histocompatibility antigen HA-1 -useful for inducing tolerance to transplants and prevent rejection or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 36; DB 20; Length 9;
88.9%; Pred. No. 9.3e+05;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minor histocompatibility antigen HA-1 T-cell epitope #1
                                                                                                                                      Hunt DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW99195 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 39; 57pp; English.
                                                                                                                                      Goulmy EAJM,
97EP-0202303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-NL00425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 88.9
                                                             UYLE-; RIJKSUNIV LEIDEN
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                                                                                                                                              The present sequence represents a new peptide (P1) constituting a T-cell epitope obtainable from the minor histocompatibility antigen H4-1. The peptide is immunogenic and can be used as part of a vaccine. P1 is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with home marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                       A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Typing minor histocompatibility antigen HA-1 - by amplifying and identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection of genetic aberrances
                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Intron, minor histocompatibility antigen HA-1; typing allele, H allele; R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant; severe aplastic anaemia; leukaemia;
                                                                                                                                                                                                                                                                                                             80.0%; Score 36; DB 20; Length 9; 88.9%; Pred. No. 9.3e+05; i. Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "not specified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "not specified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "not specified"
Engelhard VH, Goulmy EAJM, Hunt DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97373 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide epitope of HA-1 antigen.
                                                                                                                    Claim 1; Page 32; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98EP-0870125.
97EP-0202303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                                                                                              Local Similarity 88.9
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-142960/12.
                             WPI; 1999-153312/13
                                                                                                                                                                                                                                                                                                                                                                           1 VLHDDLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                    9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                             Matches
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                                         histocompatibility antigen HA-1. The specification describes methods for typing alleles (preferably the H and R alleles) of the minor histocompatibility antigen HA-1 in a sample, which comprise detecting polymorphic nucleotides in the CDNA or genomic nucleic acids of the alleles. The methods can be used for HA-1 typing for bone marrow transplants, severe aplastic anaemia, leukaemia and immune deficiency diseases, as well as detection of genetic aberrances. The probes and primers of the invention can be used to screen for the HA-1 alleles. The HA-1 peptides can be used anti-idiotypic B cells and/or T cells and antibodies.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing a cytotoxic T lymphocyte response - by maintaining a level of antigen in the lymphatic system of a mammal so as to provide a sustained CfL response, used to treat, e.g. AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                             66.7%; Score 30; DB 20; Length 9; 66.7%; Pred. No. 9.3e+05; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T cell epitope/MHC ligand SEQ ID NO:52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 25; 199pp; English.
                Example 1; Page 22; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY10122 standard; Peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-JS14289.
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97CA-2209815.
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  1 VLHDELLEA
                                                                                                                                                                                                                                                                                                                                                                                                      VXHDDXXEA
                                                                                                                                                                                                                                                             9 A.A.;
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                                                                                                                                                                                                                                                               Sequence
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Gaps

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DB 23; Len. 9.3e+05;

62.2**%**; 83.3**%**;

5; Conservative

1 VLHDDL 6

Query Match Best Local Similarity Matches 5; Conserv

9 A.

Seguence

Mismatches Score 28; Pred. No.

The invention relates to a method of inducing and/or sustaining an immunological cyctoxic T lymphocyte (CTL) response in a mammal comprising administering directly to the lymphatic system of the mammal:

(a) an antigen in the form of a polypeptide; (b) a vector comprising an uncleic acid encoding the antigen; or (c) a non-peptide antigen. The method is useful for inducing and/or sustaining CTL response in a mammal. This is particularly useful for treating a mammal having a malignant tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious disease (e.g. heptritis, acquired immune deficiency syndrome (AIDS), malaria, measles or tuberculosis), or in an animal having a predisposition to these diseases. The mammal may be dogs, cats, mice, cattle, sheep, pigg, goats, rabbits, or preferably humans.

ABG79753-ABG80319 represent viral epitopes on major histocompatibility complex (MHC) class I molecules, used in the method of the invention. Disclosure; Page 19; 73pp; English. 15-NOV-2002 Kundig TM, Sequence Query Match ABG79805; Best Loc Matches RESULT 9 ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system;
              e.g. viral disease such as heparatis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes place in the milleu of the lymphoid organ, and it sustains stimulation that is necessary to keep CTL active, cytotoxic and recirculating through the body. AAV10071 to AAV10639 represent examples of peptide antigens given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Major histocompatibility complex, MHC; MHC class I molecule; virus; epitope; cytocoxic T lymphocyte response; CTL response; lymphatic system antigen; immunogenic; malignant tumour; carcinoma; melanoma; leuxaemia; lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis; acquired immune deficiency syndrome; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing or sustaining immunological cytotoxic Tlymphocyte response a mammal, useful for treating a mammal with malignam tumour or infectious disease, by directly administering an antigen to the Tymphatic system of the mammal
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                               DB 20; Lem
. 9.3e+05;
C;
                                                                                                                                                                                                                                                                                                                                               Xismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHC class I molecule, viral epitope #53.
                                                                                                                                                                                                                                                                                      Score 28;
Pred. No.
disease such as cancer, e.g. malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG79805 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CTLI-) CTL IMMUNOTHERAPIES CCRP.
                                                                                                                                                                                                                                                                                      62.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-2002; 2002WO-US02033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-2001; 2001US-0776232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-657536/70.
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epstein Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                 1 VLHDDL 6
                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VLHEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WOZ00262368-A2
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Artirheumatic, antiallergic, antiarthritic, nootropic, neuroprotective, estimatory, major histocompatibility complex, MHC. autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis, rheumatoid arthritis, neurodegenerative disorder; Alzheimer's disease;

MHC binding peptide SEQ ID No 280.

10-APR-2003 (first entry)

ABJ20115;

ABJ20115 standard; Peptide; 9 AA.

RESULT 10

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inflammation; gene therapy; MHC binding peptide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. Alzheimer's disease, or diseases associated with inflammation. The sequences of the invention may be used in a gene therapy application. This sequence represents a peptide relating to the method for identifying MHC binding peptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            originating from a particular cell type, which are capable of binding to major histocompatibility complex (MHC) molecules of a particular haplotype. The method comprises analysing peptides bound to the soluble and secreted form of the FMC molecules of the particular haplotype. The method is useful for identifying peptides for treating an autoimmune disease, such as T or B cell and/or allergic disease or condition, rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method for identifying peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 24; I
Pred. No. 9.3e+05;
I; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 58; Page 215; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLHDD 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCHTI I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
8
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Identifying peptides that are capable of binding to major histocompatiblity complex (MHC) molecules of a particular haplotype by analyzing peptides bound to the soluble and secreted form of the MHC molecules of the particular haplotype.

Buchsbaum

Dassau L,

Admon A,

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Beer I,

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Barnea

WPI; 2003-210043/20.

(TECR) TECHNION RES & DEV FOUND LTD.

:6-MAY-2002; 2002WO-IL00383. 16-MAY-2001; 2001US-290958P. 29-MAY-2001; 2001US-0865548.

WO200294981-A2.

28-NOV-2002

Unidentified.

Faul J;

AAE31275;

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× XX

AAE3127

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The specification describes an assay for screening and identifying pharmaceutically effective compounds that specifically interact with an and modulate the activity of a cellular receptor or ion channel. The assay uses a mixture of recombinant cells, each comprising a receptor or interaction with an extracellular signal, a recombinant gene encoding interaction with an extracellular signal, a recombinant gene encoding a potential receptor polypeptide, and a reporter gene construct. The assay is useful for rapid screening of large numbers of polypeptides to identify polypeptides are agonizing or agonizing receptor activity, and confirm to identify ligands for orginal receptors, especially ligands or orginal receptors, especially ligands or orginal receptors, especially ligands for companies or the G-alpha subunit the assay of the invertion can be used to delineate the determinants involved in G-alpha-G-betagamma association.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification of compounds modulating cellular receptor activity useful for identifying and screening for ligands for orphan receptors, comprises using recombinant cells comprising both receptors and test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein coupled receptor; GPCR; cellular receptor; ion channel; surrogate ligand; orphan receptor; G-alpha subunit; GPA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy AJ, Fowlkes DM, Broach J, Manfredi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%; Score 25; DB 22; Length 9; 33.3%; Pred. No. 9.3e+65; Lindels ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide fragment of yeast G-alpha subunit (GPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 17, 50pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB84492 standard; peptide; 9 AA.
                                                                                                                                                                96US-0582333.
93US-0041431.
94US-0190328.
94US-0303133.
95US-0461383.
95US-0461389.
                                                                                                                          21-EEC-2000; 2000US-074774
                                                                                                                                                                                                                                                                                                                                         95US-0464531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   (CADU-) CADUS PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-615870/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VLHODILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: |: |: |: |: | 1 LIHEDIAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 A.
                                     US2001026926-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                Trueheart J;
                                                                                                                                                                                                                                                                         05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                   20-SEP-1994;
                                                                                  04-OCT-2001.
                                                                                                                                                                                        31-MAR-1993,
                                                                                                                                                                                                                 31-JAN-1994
                                                                                                                                                                                                                                                           13-0CT-1994;
                                                                                                                                                                                                                                                                                                                                           05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                         Klein CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA384492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for providing, identifying or/and optimising peptides which induce cycotoxic T-lymphocytes and to the uses of the obtained peptides for vaccination. The method is useful for providing, identifying and/or optimising peptides that are useful in manufacturing a pharmaceutical composition for the induction of cytocoxic T-lymphocytes, and for the prevention, treatment or diagnosis of cancer or viral infections. The invention is also used in gene therapy. The present sequence is human mageB peptide used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Providing, identifying or optimizing peptides for inducing cytotoxic T-lymphocytes and for treating cancer, comprises selecting conserved regions in antigenic proteins and identifying CD8+ T-cell epitopes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                       Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellular receptor; ion channel; cellular activity; drug discovery; orphan receptor ligand; G-alpha subunit; GPA1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 23; Length 9;
Pred. No. 9.3e+05;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filter M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino terminal of the G-alpha subunit (GPA1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eichler-Mertens M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG79144 standard; peptide; 9 AA.
                                                                                  AAE31275 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-2001; 2001US-274250P.
14-MAY-2001; 2001US-290353P.
18-MAY-2001; 2001US-291610P.
                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAR-2002; 2002WO-EP02666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.8
Best Local Similarity 37.5
Matches 3, Conservative
                                                                                                                                                                                                               Human mageB peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CALL-) CALLISTOGEN AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | | : : : 1 ILHDKIID 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wrede P, Walden P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : VLHDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-759836/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
                                                                                                                                                                                                                                                                                                                                           WO200272627-A2
                                                                                                                                                                                                                                                                                                   Home sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-2002
                                                                                                                                                                    24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the protein
                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-2002
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Seguence

RESULT 12 AAG79144 ID AAG7

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 $X \times X \times X$

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Gaps

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The invention relates to a recombinant yeast cell having an endogenous yeast pheramone system pathway and comprising a heterologous G protein coupled receptor which functionally couples to the pathway and a mutation which renders an endogenous yeast Stp22 protein non-functional. The recombinant yeast cell exhibits enhanced sensitivity to ligandinice of protein stimulation and is used for identifying compounds that modulate a G protein coupled receptor. It is useful in drug screening assays. The present sequence is yeast GPA1 amino terminal peptide used
                                        Recombinant yeast cell having enhanced sensitivity to ligand-induced G-protein stimulation for use in drug screening assays, comprises a heterologous G protein coupled receptor and a mutated stp22 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypertension, myocardial infarction, congestive heart failure, endetoxic shock; subarachnoid haemorrhage; asthma, arrhythmias, acute renal failure; precelampsia, diabetes; metabolic; endocrinological, neurological; disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide(s) used as endothelin antagonists - for treating hypertension, metabolic and endocrine disorders, heart failure,
                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                 Score 25; DB 23;
Pred. No. 9.3e+05;
; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetes, asthma, neurological disorders, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor MD;
                                                                                                        Disclosure, Column 51-52; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ]
/note= "Ac-D-His"
                                                                                                                                                                                                                                                                                                                                                                                                                             AAR29358 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 86; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doherty AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endothelin antagonist peptide.
                                                                                                                                                                                                                                                                                    55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                              3; Conservative
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                WPI; 2002-461611/49
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LIHEDIAKA
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      1 VLHODILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Depue P,
                                                                                                                                                                                                                                                             9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xey
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-1991;
18-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9220706-AL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR29358;
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                                                                                display
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
AAR29358
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                                                                                                                                                                                                                                                                                                                    The specification describes a method for identifying a ligand for an orphan G protein coupled receptor (GPCR). The method comprises rapidly screening large numbers of polypeptides in a yeast expression library to identify those polypeptides which induce or antagonise receptor bioactivity. The method is useful for screening and identifying pharmaceutically effective compounds that specifically interact with assay is particularly amenable for identifying surrogate ligands for orphan receptors. The present sequence represents a peptide derived from a yeast G-alpha subunit (GPA).
                                                                                                                                                                                                                                                        Identifying a ligand for an orphan G protein coupled receptor comprises using an recombinant yeast expression library -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGED
                                                                                                                                                                                            Paul J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant yeast cell; G protein coupled receptor; Stp22 protein; drug screening; yeast; GPA1.
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                                                                                                                                                                                            Manfredi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jength 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 22; Len
Pred. No. 9.3e+05;
                                                                                                                                                                                            Broach J,
                                                                                                                                                                                                                                                                                             Disclosure, Column 31, 128pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast GPA1 amino terminal peptide #2.
                                                                                                                                                                                            Murphy AJM, Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE26631 standard, peptide, 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
                                                                                     93US-0041431.
94US-0190328.
94US-0309313.
94US-0322137.
95US-0463181.
                                                                96US-0582333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                 (CADU-) CADUS PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CADU-) CADUS PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ostanin K, Silverman L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VLHDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                 WPI; 2001-396979/42
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LIHEDIAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 A.
                                                                                                  31-JAN-1994;
20-SEP-1994;
13-OCT-1994;
05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6355473-B1
                                                                                                                                                                                                        Trueheart J;
             US6255059-B1
                                                              17-JAN-1996;
                                                                                         31-MAR-1993;
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                                                                                                                                                                                            Kleir CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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Gaps

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The peptide is an endothelin antagonist useful in controlling hypertension, myocardial infarction, congestive heart failure, endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal failure, preeclampsia, diabetes and metabolis, endocrinological and neurological disorders. Administration is oral parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/day. It may be prepared by conventional peptide synthesis. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 6 AA;

Gaps .. 0 Query Match 53.3%; Score 24; DB 13; Length 6; Best Local Similarity 60.0%; Pred. No. 9.3e+05; Matches 3; Conservative 2; Mismatches 0; Indels

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Search completed: October 20, 2003, 13:45:47 Job time : 58 secs

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Query Match
Best Local Similarity
Matches 4; Conserv
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US-10-166-225A-163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No, is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                   October 20, 2003, 13:48:32 ; Search time 43 Seconds (without alignments) 34:308 Million cell updates/sec
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1: /cgn2 6/prodata/2/pubpaa/USG7 PUBCCMB.pep: *

2: /cgn2 6/prodata/2/pubpaa/USG7 NEW PUB.pep: *

3: /cgn2 6/prodata/2/pubpaa/USG6 NEW PUB.pep: *

4: /cgn2 6/prodata/2/pubpaa/USG6 PUBCCMS pep: *

5: /cgn2 6/prodata/2/pubpaa/USG6 PUBCCMS pep: *

6: /cgn2 6/prodata/2/pubpaa/USG8 PUBCCMS.pep: *

7: /cgn2 6/prodata/2/pubpaa/USG8 PUBCCMS.pep: *

9: /cgn2 6/prodata/2/pubpaa/USG8 PUBCCMS.pep: *

10: /cgn2 6/prodata/2/pubpaa/USO8 PUBCCMS.pep: *

10: /cgn2 6/prodata/2/pubpaa/USO8 PUBCCMS.pep: *

10: /cgn2 6/prodata/2/pubpaa/USO9 PUBCCMS.pep: *

10: /cgn2 6/prodata/2/pubpaa/USO0 PUBCCMS.pep: *

10: /cgn2 6/prodata/2/pubpaa/USO PUBCCMS.pep: *

10: /cgn2 6/prodata/2/pubca/USO PUBCCMS.pep: *

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-166-225A-164
US-10-166-225A-165
US-10-166-225A-166
US-10-166-225A-166
US-10-166-225A-162
US-10-267-074-14
US-10-267-074-14
US-10-267-074-16
US-10-020-353-364
US-09-982-172-74
US-09-982-172-74
US-09-984-765-132
US-09-984-765-132
US-09-984-765-132
US-09-984-765-132
US-09-984-765-132
US-09-984-765-132
US-09-984-765-132
US-09-984-765-132
US-09-911-838-156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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length: 9
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Perfect score:
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Maximum DB s
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                                                                                                                                                                                                              Run on:
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      155, App

157, App

167, App

168, App

168, App

170, App

170, App

170, App

1716, Ap
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                                 Sequence Seq
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US-10-166-225A-163
Sequence 163, Application US/10166225A
Publication: No. USSC030148416A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BRETZEL, Werner
APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELL, Markus
APPLICANT: HUMBELL, Markus
APPLICANT: HUMBELL, Anne F.
TITLE OF INVENTION: INPROVED ISOPRENOID PRODUCTION
TITLE OF INVENTION: UNRROVED ISOPRENOIS
FILE REFRENCE: OB435/L2166
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 2022-06-05
NUMBER OF SEQ ID NGS: 197
US-09-911-838-155
US-09-911-838-157
US-10-101-469-86
US-10-001-469-453
US-10-001-469-453
US-10-001-469-453
US-10-001-469-453
US-10-001-469-453
US-10-001-469-1022
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US-10-001-469-1022
US-10-001-469-1022
US-10-001-469-1036
US-10-101-469-1036
US-10-101-469-1036
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US-10-101-469-1036
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US-10-166-225A-164
; Sequence 164, Application US/10166225A
; Publication Nc. US20030148416A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                         Query Match 57.8%; Score 26; DB 12; Length 6; Best Local Similarity 80.0%; Pred. No. 5.4e+05; Matches 4; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEBLLT 5
US-10-166-225A-161
Sequence 16., Application US/10166225A
Publication No. US20030148416A1
CUNERAL INFORMATION:
APPLICANT: SERRY Ala:
APPLICANT: BERRY Ala:
APPLICANT: BERRY Ala:
APPLICANT: LOPEZ-ULIBARRI, Rual
APPLICANT: LOPEZ-ULIBARRI, Rual
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER F.
APPLICANT: MAYER F.
CURRENT APPLICATION NUMBER: US/10/166,225A
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US-10-166-225A-162
Sequence 162, Application US/10166225A
Publication No. US2003C148416A1
GENERAL INCRAMATION:
APPLICANT: BERRY, Alan
APPLICANT: BERRY, Alan
APPLICANT: LOPEZ-ULIBARR, Rual
APPLICANT: LOPEZ-ULIBARR, Rual
APPLICANT: MARKE, Anne F.
APPLICANT: WEISEEV Alexei A.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
TITLE OF INVENTION: UMPRER: US/10/166,225A
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT APPLICATION NUMBER: US/10/166,225A
SOFTWARE: PatentIn version 3.1
SEQ ID NO 162
LENGTH: 6
MARKET APPLICATION VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Rhizobium sp. strain NGR234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Bradyrhizobium japonicum
NUMBER OF SEQ ID NOS: 197
| SOFTWARE: ParentIn version 3:1
| SEQ ID NO 165
| LENGTH: 6
| TYPE: FRT ORGANSM: Haemophilus influenzae
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| IHDD2 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
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Pred. No. 5.4e+05;
1; Mismatches 0; Indels
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Sequence 165, Application US/10166225A

Publication No. US25030148416A1

GENERAL INFORMATION:
APPLICANT: BERTY Alan
APPLICANT: HUMSELN, Markus
APPLICANT: HUMSELN, Markus
APPLICANT: HUMSELN, Markus
APPLICANT: YELISEEV, Alexel A.
TITLE OF INVENTION: INFOVED ISOPRENOID PRODUCTION
FILE REFERENCE: C38445/121966
CURRENT FILING DATE: 2002-06-05
NUMBER OF ESD ID DATE: 2002-06-05
NUMBER OF ESD ID NOS: 197
SEQ ID NO 165
FERENCE: ABROWNED OF SECOND NOS: 197
SEQ ID NO 165
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Publication No. US20030148416A1
GENERAL INFORMATION:
APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Markus
APPLICANT: HUMBELIN, Markus
APPLICANT: LOPEZ ULIBARRI, Rual
APPLICANT: YELISEEV, Alexei A.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REPERENCE: C38435/121966
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 2002-06-05
APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Markus
APPLICANT: LOPEZ-ULIBARI, Rual
APPLICANT: LOPEZ-ULIBARI, Rual
APPLICANT: MAYER, Anne F.
APPLICANT: YELISEEV, Alexei A.
TITLE OF INVENTION: IMPROVED ISOPRENCID PRODUCTION
FILE REFERENCE: C38435/121966
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 164
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRGANISM: Escherichia coli
US-10-166-225A-165
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Best Local Similarity 80.0
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Best Local Similarity 80.0
Matches 4, Conservative
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US-10-267-074-16

US-10-267-074-16

Sequence 16, Application US/10267074

Publication No. US2030108999A1

GENERAL INFORMATION:
APPLICANT: Mandred, John
APPLICANT: Mendy-Yu
APPLICANT: Mendy-Yu
APPLICANT: We, Mendy-Yu
TITLE OF INVENTION: RESPONSES:
TITLE OF INVENTION: AND USSS THEREFOR
FILE REPRENCE: CPP-08

TITLE OF INVENTION: AND USSS THEREFOR
FILE REPRENCE: CPP-08

CURRENT APPLICATION NUMBER: US/10/267, D74

CURRENT FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 18

SOSTWARE: PRICET: 1999-08-20

NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: CONSENSUS MOTIFUS-10-267-074-14
                                                                                                                                                                                                                                                                                                                                                                Saps
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US-10-267-274-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.6%; Score 25; DB 15; Length 9; 33.3%; Pred. No. 5.4e+05; Live 5; Mismatches 1; Indels
                  FILE REPERBNCE: CPI-088
CURRENT APPLICATION NUMBER: US/10/267,074
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/378,046
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 18
SCFTPARE: Patentin Ver: 2.0
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.3
Matches 3; Conservative
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: LIHEDIAKA 9
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: LIHEDIAKA
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Matches 3, Conserv
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                                                                                                                                                                               LEWGTH:
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Publication No. US20030108999A1
GENERAL INFORMATION:
APPLICANT: Manfredi, John
APPLICANT: Manfredi, Benjamin K.
APPLICANT: Wu, Meny-Yu
APPLICANT: Wu, Meny-Yu
ITLE OF INVENTION: CELLS HAVING AMPLIFIED SIGNAL TRANSDUCTION PATHWAY
TITLE OF INVENTION: RESPONSES
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                    0; Indels
                                                                                                                                                                                                                                                                               Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for Identifying Receptor Effectors
80.0%; Fred. No. 5.4e+05;
ive 1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUX TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION UNMERR: US/09/953,354
FILING DATE: 13-Sep-2601
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/689,172
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-953-354-3
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSES: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                          APPLICANT: Klein, Christine A.
                                                                                                                                                                                               Sequence 3, Application US/09953354 Publication No. US20030054402Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3
Matches 3; Conservative
                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VLHDDLLEA 9
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EIHEDIAKA
Best Local Similarity
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                                                                                                                                                                               US-09-953-354-3
                  Matches
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Sequence 30, Application US/0933497B
Parent No. USCUSO0941934.
GENERAL INFORMATION:
APPLICANT: Ward, Sizabeth S.
TITLE OF INVENTION: IMMUNOGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
FILE REPREMENE: USFD143
CURRENT APPLICATION NUMBER: US/09/933,497B
CURRENT FILING DATE: 2002-02-07
FRIOR APPLICATION NUMBER: 60/013,563
FRIOR RILING DATE: 1996-03-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 33
                                                                                                                                                                                              Gaps
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                                                                                                                                                                                              <u>ن</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:
APPLICANT: Mary Paris
APPLICANT: Arthur Paris
APPLICANT: Arthur Paris
APPLICANT: Arthur Paris
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: GTP-BINDING PROTEIN USEFUL IN TREATMENT
ITILE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
FILE REFRENCE: 129.6031
CURRENT APLICATION NUMBER: 05/09/467
PRIOR APPLICANTION NUMBER: 6/197,647
PRIOR APPLICANTION NUMBER: 6/197,647
PRIOR FILING DATE: 2000-64-12
NUMBER OF SEC ID NOS: 770
SOFTWARE: PSEUSEC for Mindows Version 4.0
SED ID NO 349
LENGTH: 3
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                                                                                                                            Cuery Match 51.1%; Score 23; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 5.4e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.9%; Score 22; DB 9; Length 5; 80.0%; Pred. No. 5.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 349, Application US/09834765 Patent No. US20020055478A1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; CRGANISM: Homo sapiens
US-09-834-765-349
) TYPE: PRT
) ORGANISM: Homo sapiens
US-09-834-765-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Best Local Similarity
Matches 5, Conserv
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Sequence 74, Application US/09982172

Patent No. US20020137119A1

GENERAL INFORMATION:

TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND ANTIBODIE

TITLE OF INVENTION: UTLIZING EACH

FILE REPERRNCE: 0./22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2301-10-19

SOFTWARE: Patentin version 3.1

SETOID NO 74
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APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
APPLICANT: Area Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE OF INVENTION: AND DETECTION OF CANCER
FILE REPERENCE: 129 64501
CURRENT APPLICATION NUMBER: 60/197,647
PRIOR APP
                                                                                                                                                                                                                                                                                                                                              Score 24, DB 12; Length 7;
Pred. No. 5.4e+C5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.1%; Score 23; DB 10; Length 8; 50.0%; Pred. No. 5.46+05; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
. OTHER TRORMATION: Computer generated synthetic peptide
US-09-982-172-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/238,760
FRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 86
LENGTH: 7
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Patent No. US20020055478A1
GENERAL INFORMATION:
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71.4%;
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-020-354-86
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JS-09-982-172-74
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RESULT 15
US-09-911-838-156
US-09-911-838-156
Sequence 156, Application US/39911838
Patent No. US2002015.6784.
GENERAL INFORMATION:
APPLICANT: ARLINGHAUS, RALPH
TITLE OF INVENTION: PROPHYLAX:S AND THERAPY OF ACQUIRED TYMUNOBERCIENCY
TITLE OF INVENTION: SYNDRCMS
FILE REFRENCE: UTSC.267USC)
CURRENT APPLICATION NUMBER: US/39/911,838
PRIOR PILING DATE: 2011-07-24
PRIOR FILING DATE: 1992-02-13
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 156
LENGTH: 6
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; CTHER INFORMATION: Description of Artificial Sequence: Synthetic
; CTHER INFORMATION: Peptide
US-09-911-838-156
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Best Local Similarity 33.3%; Pred. No. 5.4e+05;
Matches 2; Conservative 4; Mismatches 0; Indels
i; Indels
0; Mismatches
4; Conservative
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Matches
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Search completed: October 20, 2003, 14:01:22 Job time: 44 secs

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                                                                                                                                                                          ) Search time 20 Seconds (without alignments) 19.040 Million cell updatos/sec
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Sequence 7, A
Sequence 8, A
Sequence 8, A
Sequence 3,70,
Sequence 3,70,
Sequence 3,70,
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Sequence 2
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Sequence 1
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/cgn2_6/ptodata/2/iaa/5B_COM3.pep:*
/cgn2_6/ptodata/2/iaa/6A_COM3.pep:*
/cgn2_6/ptodata/2/iaa/B_COM3.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COM8.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COM8.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - protein search, using sw model
                                                                                                                                                                             October 20, 2003, 13:43:56
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Gapop 10.0 , Gapext 0.5
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 9
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Perfect score:
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                                                                                                                     CM protein
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No.
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Gaps
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                                                                                                                                                CONSUTER READMED FORM

CONSUTER: Eloppy disk

CONSUTER: IBW PC Compatible

CORRENT APPLICATION PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NOMER: US/09/803,951

FILING DATE: 1-Mar-2001

CLASSIFICATION: CURNOWN-

PRICE APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NOMER: 09/025,819

FILING DATE: CURNOWN-

ATTORNEY/AGENT INFORMATION:

KAAME: KABAILISET, HORIT:

RECHERENCE/DOCKET WUNBER: 10235/2

TELEPHONE: 202-220-4201

INFORMATION FOR SEQ IE NO: 5:

SEQUENCE CHARACTERISTICS:
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JOHNERAL INFORMATION:
APPLICANT: Michin, Christine A.
APPLICANT: Murphy, Andrew C. M.
APPLICANT: Murphy, Andrew C. M.
TILLE D'E INVENTION: Methods and Compositions for TILLE D'E INVENTION: Identifying Receptor Effectors NUMBER CF SQUENCES: 98
CORRESPENDINCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,333A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CACHERING IN ARAB
REGISTRATION NUMBER: 41,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
ZIP: 02:19-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELOppy disk
COMPUTER: ELOppy disk
COMPUTER: ELOppy DISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
TCPOLGGY: linear
                                                                                                             ZIP: 20005
CCMPUTER READABLE FORM:
ADDRESSEE: KENYON
STREET: 1500 K Str
CITY: Washington
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US-08-582-333A-3
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TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    APPLICANT: Obata, Shusei
Nishino, Tokuzo
Koyama, Tanetoshi
Sato, Yoshihiro
TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
CORRESPONDENCE: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005

COMPUTER READABLE FORX:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DCS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/09/808,126

FILING DATE: 08-May-2001

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.6%; Score 25; DB 4; Length 7; 80.0%; Pred. No. 2.5e+05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION NUMBER: 09/025,819
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Khalilian, Hour:
REFERENCE/DOCKET NUMBER: 10235/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-808-126-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-803-951-5
Sequence 5, Application US/09803951
Parent No. 6433761
GENERAL INFORMATION:
APPLICANT: Obata, Shusei
Nishino, Tokuzo
Vovama, Tanetoghi
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: KENYON & KENYON STREET: 1500 K Street, N.W
                                                                                                                                                      Sequence 5, Application US/03808126
Patent No. 6410280
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
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Best Local Similarity 80.0
Artches 4; Conservative
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COUNTRY: USA
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Patent No. 6174715
GENERAL INFORMATION:
APPLICANT: YURAMATSU, Masayoshi
APPLICANT: YORK, Ayuni
APPLICANT: KOYAMA, KYOZO
APPLICANT: KOYAMA, KYOZO
APPLICANT: SHINKZU, Naoto
APPLICANT: SHINKZU, Naoto
APPLICANT: CHO, Yenwin
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
VUYBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ALDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23, DB 3, Length 6, Pred, No. 2.5e+05, 2, Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALURESSBE: Kenyon & Renyon
STREET: 1025 Connecticut Avenue, NM - Suite 600
CIIY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
COUNTRY: US
COUNTRY: US
CAPUTER READBLE FORM:
MEDIUM TYPE: 3.5 Inch Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WORDPE-fect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,235B
FILING DATE: 11-Jun-1997
CLASSIFICATION 435
PRING APPLICATION DATA:
APPLICATION NUMBER: UP 154441/1996
FILING DATE: 14-Jun-1996
ATTORNEY AGENT INFORMATION:
MEDIUM TYPE: 1.5 inch Floppy disk COMPUTER: IBM PC compatible CPERATING SYSTEM: PC-DOS/MS-DOS 6.2 SCFFWARE: WordPerfect 6.1 for Windows CURRENT APPLICATION NUMBER: US/03/217,609A
                                                                                                                                                                  CLASSIFICATION:
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/873,235
FILING DATE: 11-Jun-1997
ATTCRNEY/AGENT INFORMATION:
NAME: TOFFENETI, Cudith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 10235/1
TELEPCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: TOFFENETTI, Judith L. REGISTRATION NUMBER: 39,048
REFERENCE FOCKET NUMBER: 10235/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-217-609A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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| GGHIT 2
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US-08-873-235B-8
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Sequence 7, Application US/C9305923A

Parent No. 6355473

Sequence 7, Application US/C9305923A

Septicant: Ostanin, Kirili

APPLICANT: Silverman, Lauren

TITLE OF INVENTION: YEAST CELLS HAVING MUTATIONS IN Stp22 AND USES THEREFOR

TILE REPERENCE: CPI-091

CURRENT APPLICATION NUMBER: US/09/305,923A

CURRENT PILING DATE: 1999-05-06

PRIOR FILING DATE: 1998-05-06

NUMBER OF SEQ ID NOS: 9

SOFTUMER: Patentin Ver. 2.0

SEQ ID NO 7

LENGTH: 9
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Patent No. 6071733
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: CGURA, Kyozo
APPLICANT: CGURA, Kyozo
APPLICANT: CHO, Yenwin
ITTLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
VUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                   Query Match 55.6%; Score 25; DB 3; Length 9; Best Local Similarity 33.3%; Pred. No. 2.5e+05; Matches 3; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.6%; Score 25; DB 4; Length 9; 33.3%; Pred. No. 2.5e+05; Live 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1025 Connecticut Avenue, NW - Suite 600
                      REFERENCE/DOCKET NUMBER: CPI-012CP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-305-923A-7
                                    TELECOMMUNICATION INFORMATION:
TELEPHCNE: (617)227-7400
TELEFAX: (617)227-4214
INFORMATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGIH: 9 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 55.6' Best Local Similarity 33.3 Matches 3: Conservative
                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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COMPUTER READABLE FORM:
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1025 Conn.
11Y: Washington STATE: DC COUNTRY: INC.
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1 LIHEDIAKA 9
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US-09-217-609A-8
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US-09-305-923A-7
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Gaps

seqla.closed.rai

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APPLICANT: Ward, Elizabeth S.
APPLICANT: Ward, Elizabeth S.
TITLE OF INVENTION: IMMUNCGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
FILE REFERENCE: UTSO: 483
CURRENT APPLICATION NUMBER: US/08/811,463C
CURRENT PILING DATE: 1997-03-03
FARLIER PILING DATE: 1997-03-03
FARLIER PILING DATE: 1996-03-18
NUMBER OF SEQ ID NOS: 39
SCFTWARE: PATENT VET. 1996-03-18
SCFTWARE: PATENT VET. 2.1
SEQ ID NOS: 30
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08228036
| Patent No. 5316326
| Patent No. 53
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-08-91-463-30
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MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTROLL SYSTEM CONTROLL CORRESTING SYSTEM MS-DCS SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/03/208,036 FILING DATE: CLASSIFICATION AND MATA:
APPLICATION NUMBER: US/07/887,282 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                // Sequence 30, Application US/08811463C
/ Patent No. 6277375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8853
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                       2 LHJDLLE 8
                                                                                                                                      2 LHQDIIK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 370, Application US/08159339A

Sequence 370, Application US/08159339A

GENERAL INFORMATION:
APPLICANT: Mileo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Gete, Alessandro
APPLICANT: Gete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION 144
PRICR APPLICATION NUMBER: US 07/926,665
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-MG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Blien Lauver
RESISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECHOMENICATION INFORMATION:
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.1%; Score 23; 38 3; L
Best Local Similarity 42.9%; Pred. No. 2.5e+05;
Matches 3; Conservative 3; Mismatches 1;
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SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Diskette
IBM Compatible
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
JS-08-873-2358-8
                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best local Similarity 60.0
Matches 3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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2 LIHDD 6
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49.9%; Score 22; DB 1; Length 7; 50.0%; Pred. No. 2.5e+05; ive 3; Mismatches 0; Indels
MEDICY TYPE: Diskette, 5.25 inch, 500 kb CCMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DISPLAYWHITE CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,036
FILING DATE:
                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/887,282
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
RSSISTAMION NUMBER: 33.367
REFERENCE/DOCKET NUMBER: 33.367
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: internal fragment
CRIGINAL SOURCE:
ORGANISM: Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
REJEVANT RESIDUES IN SEQ ID NO:
US-08-208-036-9
                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
FINGTH: 7 aming acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KFY:
LOCATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME:
CHROMOSONE/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISCLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
Matches 3; Conserv
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
CEALLINE:
IMMEDIATE SOURCE:
LIBERRY:
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2 VHDELV 7
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ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VOLUME:
ISSUE:
PAGES:
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; Sequence 9, Application US/28208036
; Patent No. 5436246
; GENERAL INFORMATION:
APPLICANT: YOSHIZUM: ISHING et al.
TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR POI I TYPE
TITLE OF INVENTION: DA POLYMERASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wanderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
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                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
AVII-SENSE:
FRAGNENT TYPE: internal fragment
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-208-036-7
                                                                          7 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%
                                   INFORMATION FOR SEG ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acid r
                                                                                                            sirgle
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP FOSITION:
UNITS:
                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                          HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL JINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
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2 VHDELV 7
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JOURNAL:
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US-08-208-036-9
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REBEULT: 2.

Sequence 7. Application (S/08428623

Sequence 7. Application (S/08428623

Sequence 7. Application (S/08428623

GENERAL INFORMATION: Obstained (S/0842862)

GENERAL INFORMATION: NETHOD FOR CLONING OF A GENE FOR TITLE OF INVENTION: NETHOD FOR CLONING OF A GENE FOR SEQUENCES: 17

CONTRIBES OF SEQUENCES: 17

CONTRIBES OF SEQUENCES: 17

CONTRIBES OF SEQUENCES: 18

CONTRIBES OF SEQUENC
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                                                                            Gaps
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       FILING DATE:

SUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-428-623-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
FRAGMENT TYPE: internal fragment
ORGANISM: Thermus aquaticus
ORGANISM: Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLGGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 7 amino a TYPE: amino acid sTRANDEDNESS: sir
DOCUMENT NUMBER:
                                                                                                       : |:|:
2 VHDECV 7
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Gaps

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PEATURE: OPERATION: Description of Artificial Sequence: nuclectide OTHER INFORMATION: codon binding sequence US-09-173-941-82
                                                                                                                                                                                                                                                                                                                                        Query Match 48.9%; Score 22; DB 3; Length 7; Best Local Similarity 80.0%; Pred. No. 2.5e+05; Matches 4; Conservative 0; Mismatches 1; Indels
GENERAL INFORMATION:
APPLICANT: BARBAS, Carlos F.
TITLE CO INVENTION: ZIVE FINGER BINDING DOMAINS FOR GNN
FILE REFERENCE: NOVO081S
CURRENT APPLICATION NUMBER: US/09/173,941
CURRENT FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October 20, 2003, 13:50:06 Job time : 20 secs
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.9%; Score 22; DB 1; Length 7; S0.0%; Pred. No. 2.5e+05; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08556419C
; Sequence 14, Application US/08556419C
; Patent No. 6093549
; GRNERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Landhan, Anthony
APPLICANT: Landhan, Anthony
APPLICANT: Solution; APPLICANT: Solution;
; TITLE OF INVENTION: Huntingtin-associated protein
; TITLE OF INVENTION: Huntingtin-associated protein
; TITLE OF INVENTION: Huntingtin-associated
; CURRENT APPLICATION WINGRER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER CF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-173-941-82
; Sequence 82, Application US/09173941
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FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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Best Local Similarity 80.0%;
Matches 4; Conservative
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                                                           CLOME:
CLOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
LOCATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
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Best Local Similarity 50.0
Matches 3, Conservative
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2 WHDELV 7
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    ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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US-08-556-419-14
                                                                                                                                                                                                                                                                                                         TITLE:
JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                VOLUME:
ISSUE:
PAGES:
DATE:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 20, 2003, 13:42:21; Search time 24 Seconds (without alignments) 36.063 Million cell updates/sec Run on:

42 1 vlrddllea 9 SEOIB Title: Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

189 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	7	hypothetical prote	Рs	acrophage	a)	n A	-sel	T-cell receptor be	. 1	T-cell receptor be	acetylcholinestera	calsequestrin, fas	T-cell receptor be	T-cell receptor be	T-cell receptor be	trypsin (EC 3.4.21	'n		phag	63-15	T-cell receptor be	_	major protein anti		pilE protein - Esc	T-cell receptor be	chitin-binding pro	158% excantigen -	ferredoxin a2 - Ja
		QI	\$68004	PC4131	S20446	A60427	PHC942	140697	PT0601	PT0679	B35640	PT0533	A34026	B39040	PT0628	PT0722	PT0576	A61328	PT0557	A39841	A37027	PH0108	PT0562	330572	D60274	П	S25266	$^{\circ}$	242	3309	869165
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conopressin S - co	chlorophyll a/b-bi	dextransucrase (EC	tetrameric protein	glycine cleavage s	transaldolase (EC	neuropeptide Grb-A	neuropeptide Grb-A	calliFWRFamide 10	gamma subust of P	neuropeptide Antho	protein-glutamine	hypothetical prote	glycoprotein compo	catch-relaxing pep	triacylglycerol li
B28495	PW0002	539841	S66419	PS0253	A12872	B57444	C57444	A44787	A48360	A35779	A26209	B44510	H48394	ECYTICA	S57274
6	ca ca	2	6	2	2	9	2		2	2	2	2	2	2	7
11 26.2	12 26.2	11 26.2	11 26.2	1: 26.2	11 26.2	11 26.2	11 26.2	(7	10 23.8	10 23.8	10 23.8	10 23.8	10 23.8	10 23.8	7
30	33	3.2	33	34	35	36	37	38	33	4€	41	4.2	43	44	45

ALIGNMENTS

5,88004 hucolin, 75K chain - human (fragment) C.Species: Komo sapiens (man) C.Date: 15-Reb-1997 #sequence_revision 13-Max-1997 #text_change 17-Mar-1999 C.Accession: 868004	FEBS Lett. 175, 159-161, 1995 Affilel Hucolin, a new corticosteroid-binding protein from human plasma with structur Affeterace number: 56304; MUID:96087107; PMID:7498469 Affetersion: 568004 Afstatus: preliminary Affesidues: 1-7 <edg></edg>	<pre>Query Match Best Local Similarity 100.0%; Pred; No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 4 DDL 6 ! </pre>	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	FEBS Lett. 159, 159.161, 1995 A/Title: Hucolin, a new cortic A/Reference number: S68064, M A/Accession: S68004 A/Status: pretiminary A/Accession type: protein A/Residues: 1-7 < EBG>	Query Match Best Local Similar Matches 3, Con Qy 4 DDL 6	Ob 4 DDL 6

Accession: Petilial protein 8 [imported] - Pseudomonas aeruginosa (fragment)
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C.Species Pseudomonas aeruginosa
C.Species Beruginosa
A.Stecession: PC4131
A.Species Beruginosa
A.Species Preliminary
A.Species Beruginosa
A.Species Berugin

٠, 0; Indels Cuery Match 38.1%; Score 16; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 2.8e+C5; Matches 3; Conservative 0; Mismatches 0; Indels

; 0

Gaps

4 DCL 6 ô qq

RESULT 3

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Jacoby
Jacobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Jaces Jacoby J966 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: 140697
R;Shiuan, D; Campbell, A.
Gace 67, 263-211, 1998
Gace 67, 263-211, 1998
A;Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacto A;Accession: 140697
A;Accession: 140697
A;Accession: 140697
A;Catus: pre-liminary; translated from GS/EWBL/DBC
A;Mclecule Type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: GS;W21922; NID:g144434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theeli receptor beta chain V-D-J region (120-2K) - mouse (fragment)
C)Species: Mus musculus (touse mouse)
C)Bate: 17-Jul-1892 #sequence_revision 17-Jul-1892 #text_change 30-May-1997
C)Accession: PT0601; PT0617; PT0694
R)FReney, A.J.
C) Exp. Med. 174, 115-124, 1991
A)T11Exp. Med. 174, 115-124, 1991
A)T11Exp. Med. 174, 115-124, 1991
A)TREFERENCE number: PT0601
A)Reference number: PT0601
A)Reference number: PT0601
A)Reference number: PT0601
A)Reference number: PT0601
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0539; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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(Species: Mus musculus (fouse mouse)
(SDate: 17-Ju-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
(Accession: PT0679; PT0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A Molecule Type: mRNA
A Mosesia: 1-5 < PEB>
A Mosesia: 1-5 < PEB>
A Mosesia: 1-5 < PEB>
A Mosesia: translation not shown.
A Mosesia: 1-5 < PEB>
A Mosesia: 1-5 < PEB>
A Mosesia: translation not shown.
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 12; DB 2; Length 4;
Pred. No. 2.8e+05;
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100.0%; Pred. No. 4...
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2; Conservative
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Molecule type: DNA
Residues: 1-5 <FE2>
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Matches 2, Conserv
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R;Cones, C.M.; Paintiams, J.S.
R;Cones, C.M.; Prince, C.A.; Williams, J.S.
A;D; Hemartol. 19, 704-709, 1991
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin A;Reference number: A60427; MUID:91372335; PMID:1909970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0942
R;Gold, D.P.; Cffner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerging A;Reference number: PH0891; MUID:92078857; PMID:1836012
                                                                    C. Accession: S20446
R.Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
FEBS Lett. 299, 291-293, 1992
A. Aritile: Identification of cleavage sites involved in proteolytic processing of Pseudomd A. Reference number: S20446; MUID:92183956; FMID:1544509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 1-9 <20N>
A;Note: the sequence from the text on page 706 is inconsistent with that from page 708
C;Keywords: cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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elastase - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Specres: Homo sapiens (man)
C.Date: 12-Peb-1993 #sequence_revision 12-Peb-1993 #text_change 18-Jun-1993
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Pred. No. 2.8e+05;
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Best Local Similarity 100...
3: Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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A,Molecule type: protein
A,Residues: 1-7 <KES>
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A; Residues: 1-9 <GOL>
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Best Local S:
Matches 3,
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C.Species: Torpedo californica (Pacific electric ray)
C.Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C.Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C.Accession: A34026
R.Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.;
J. Siol. Chem. 263, 1140-1145, 1988
A.Title: Divergence in primary structure between the molecular forms of acetylcholinos A; Reference number: A34026; MUID:88087239; PMID:333534
A; Molecula type: protein.
A; Molecula type: protein.
A; Residues: 1-7 cg13>
C; Keywords: alternative splicing; carboxylic ester hydrolase
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Date: 35-Cores, L.R.
7. Eigh, S.E.; Jones, L.R.
7. Eigh, Chem, 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by case A;Reference number: A39040; MCID:91093133; PMID:1985907
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J. Exp. Med, 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUID:91277601; PMID:1711558
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C:Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: P10628
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A;Residues: 1-7 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
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A;Xolecule type: procein
A;Rosidues: 1.7 < CAL>
C;Keywords: phosphoprotein; skeletal muscle
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Sest Local Similarity 75.0%;
Matches 3; Conservative (
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CiSpedies: Mus musculus (house mouse)
CiSpedies: Mus musculus (house mouse)
CiDate: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
CiAccession: B33640
Richen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal mark
A;Reference number: A35640; MUID:90222173; PMID:2326268
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: Pr0533
R;Peeney, A.J.
C. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: Pr0509; MUID:91277601; PMID:1711558
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                        A.Molecule type: DNA
A.Residues: 1-5 <FEE>
A.Residues: 1-5 <FEE>
A.Accession: Brownes: day 18 fetal thymus, strain BALB/c, i54-23
A.Accession: Br708
A.Status: translation not shown
A.Status: ps: DNA
A.Molecule type: DNA
A.Residues: 1-5 <FEE>
A.Experimental source: newborn thymus, strain BALB/c, 161-25
C.Keywords: T-cell receptor
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A)Molecule type: mRNA
A)Residues: 1-6 <FEE>
     A;Status: translation not shown
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Best Local Similarity 66.7
Matches 2; Conservative
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A;Molecule type: mRNA
A;Residues: 1-6 <CHE>
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PT0722
T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)
C:Specias: Mas musculus (house mouse)
C:Specias: Mas musculus (house mouse)
C:Specias: Mas musculus (house mouse)
C:Accession: PT0722
C:Accession: PT0722
R:Feeney, A.J.
R:Feeney, A.J.
R:Frite: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Accession: PT0722
A:Accession: PT0722
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A.Yolecule type: DNA
A.Residtes: 1-7 <FEES
C.Xeperimental source: newborn thymus, strain BALB/c
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Best Local Similarity 100.
Matches 2, Conservative
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Pro576
Treell receptor beta chain V-D-J region (141-1G) - mouse (fragment)
Treell receptor beta chain V-D-J region (141-1G) - mouse (fragment)
Treell receptor beta chain (house mouse)
Treell receptor beta 30-May-1997
Cracession: PT0576
R.Peeney, A.J.
The Med. 174, 115-124, 1991
A.Thile: Junctional sequences of fetal Treell receptor beta chains have few N regions.
A.Reference number: PT0509; MUD:91277601; PMID:1711559
A.Status: translation not shown
A.Molecule type: mRNA
A.Residues: 1-7 cFEE>

RESULT 15

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Gaps

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Query Match
28.6%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels

Search completed: October 20, 2003, 13:49:19

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AiResidues: 1-7 <FEE> AiExperimental source: day 19 fetal thymus, strain BALB/c CiKeywords: T-cell receptor

calliphora brassica na homarus ame macrobrachi

homarus ame macrobrachi

P41486 P41487 P83277 P83275

panagrellus penaeus mon

P41863 P41863 P41856 P41856 P41873 P83276 P83319 P83320

penaeus :

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calliphora

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SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.

Somez R., Losada M., Serrano A.;

Submitted (JN-2001) to the SWISS-PROT data bank.

-- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.

-- SUBCELJALAR LOCATION: Cytoplasmic.

-- SUBCELJALAR LOCATION: Cytoplasmic.

-- SUBCELJALAR LOCATION: 2D-GEL THE DETERMINED MM OF THIS PROTEIN IS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-PB-2003 (Rel. 41, Last annotation update)
Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pid77.2,
01-J7A-1990 (Rel. 13, Created)
01-JAA-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase)
aminotransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhodopseudomonas viridis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Blastochloris.
NCBI_TaxID=1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13; DB 1; Length 9; Pred. No. 1.3e+05; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68F3EAA05DDAA044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 kDa.
SIXILARITY: Belongs to the PPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                            ALIGNMENTS
                  PAR3_HOMAM
PAR4_HOMAM
PAR8_CALVO
PLP_BRANA
PAR1_CALVO
PAR3_PAR8
PAR3_PAR82
PAR3_PAR82
PAR3_PENMO
PAR3_PENMO
PARS_PENMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP: MF 30209; -; 1.
InterPro; IPR001596; Pyrophosphatase.
PROSITE; PS00387; PPASE; PARTIAL.
FAR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.0%;
28.6%;
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9 AA; 1014 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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BICA_CITFR
ID BICA_CITFR
AC P13071;
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IPYR_RHOVI
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P24272 vibrio fisc
P56414 pseudomonas
P10420 myrilus edu
P81379 lycopersico
P81379 locusta mig
P31934 homo sapien
P42562 hirudo medi
P42561 hirudo medi
P42561 hirudo medi
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pichia jadi
vibrio fisc
anthopleura
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conus stria
panagrellus
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helisoma tr
macrobrachi
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citrobacter
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                    5.1.6
Compugen ind.
                                                                                                                                                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
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                    GenCore version (c) 1993 - 2003
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BIOA_CITFR
NSK1_SARBU
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UFA2_MOUSE
UFA2_HUMAN
UC26_MAIZE
CONO_CONST
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation, the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota, Metazca, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Oestroidea,
Sarcophagidae, Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-9308101; PubMed=1360367;
Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
Comp. Biochem. Physiol. 103C:135-142(1992).
-:- FUNCTION. MYOTROPIC PEPTIDE.
-:- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTCKININ FAMILY.
InterPro; IPRO0165; GASTRIN; 1.
Neuropeptide; Amidation; Sulfation.
MOD_RES 4 4 A SULFATION (POTENTIAL).
MOD_RES 9 AMIDATION (POTENTIAL).
SEQÜENCE 9 AA; 1187 MW, 8BOA0691E86BSAAA CRC64;
                                                                                                                                                                                                                                                                                                               PATHWAY: Biotin biosynthesis.
SUBUNIT: Homodimer.
SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent aminotransferases.
                             Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Trobaccer freundii and Salmonella typhimurium bictin operons.";
Gene 67:203-211(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                      CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
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100.0%; Pred. No. 1.3e+05;
trive 0; Mismatches 0;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last arnotation update)
Neosu-fakinin-1 (NEB-SK-I)
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                                                                                                                                                                                                                                                                             COFACTOR: Pyridoxal phosphate.
PubMed=2971595
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Best Socal Similarity 190.
Matches 2; Conservative
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Matches 2; Conservative
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ID NSK1_SARBU
AC P41492;
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-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- FM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its (
terminal amidation.
-!- MASS SPECIFICATION: MM-883; METHOD=FAB.
Amphibian defense pepilde; Amidation.
Amphibian defense pepilde; Amidation.
SEQUENCE 9 AA, 884 MW; 2C2D77205AA72728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skin secretion;
Wabhitz P.A., Boyle J.H., Tyler M.J., Wallace J.C.;
Wabhitz P.A., Boyle J.H., Tyler M.J., Wallace J.C.;
Wabhitz From the skin glands of the Australian buzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                Bukaryota, Xetazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura; Neobatrachia, Bufonoidea, Hylidae,
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUSE. J. Chem. Servarious and properties activity nor antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The structure of new peoplides from the Australin red tree frog 'Licoria rubella'. The skin peotlide profile as a probe for the of evolutionary trends of amphibians.";
Aust. C. Chem. 49:955-961(1996).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND MASS SPECTROMETRY.
TISSUBE-Skin accretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-FB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.6%; Score 12; DB 1; Length 9; 66.7%; Pred, No. 1.3e+05; tive 1; Mismatches 0; Indels
                                                                                                                               9 AA.
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MEDLINE=95009907; PubMed=7523108;
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rubella.";
7. Chem. E
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P38640;
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-!- MISCELLANEOUS: ON THE 20-GEL THE PROTEIN IS: 7.0, ITS WW IS: 57.2 Maize-20PAGE; P80632; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus striatus (Striated cone)
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2, Conserva
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Best Local &
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P82661;
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDIINE=95203287; FubMed=7895732;
Corbett J.X., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn X.J.;
"The human myocardial two-dimensional gel protein database: update 1994.";
                     using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745/1994).
-!- MISCELLANDOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Electrophoresis 15:1459-1465(1994).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
NON TER
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Spermatophyta, Magnollophyta, Liliopsida, Poales, Foaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
WCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eureleostomi,
Mammalia, Butheria, Primates, Cararrhini, Hominidae, Homo.
NCSI_TaxID=9606;
    Separation and sequencing of familiar and novel murine proteins
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ID UCZ6_MAIZE

STANDARD; PRT; 8 AA.

D UCZ6_MIZE

DT 01-0CT-1996 (Rel. 34, Created;

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

D URNOWN PROTEIN From 2D-page of etiolated coleoptile (Spot 907)
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Ol-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Unknown protein (Ren. 2D-page of heart (Spot 5603) (Fragment).
Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%; Score 12; DB 1; Length 9; 100.0%; Pred. No. 1.3e+C5; Exve 0; Mismatches 0; Indels
                                                                                                                                                                    Score 12, DB 1, Length 9, Pred. No. 1.30+35; Mismatches 1, Indels
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                                                                                                                             9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  9 A.A.
                                                                                                                                                                                                               3, Mismatches
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Theor. Appl. Genet. 93:997-1005(1996)
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                    28.6%;
20.0%;
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity
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1 MEDEI 5
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SEQUENCE
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UHA2_HUMAN
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DETERMINED PI OF THIS UNKNOWN KDa.
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Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms."; J. Biol. Chem. 262:15821-15824 (1987).
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Concidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89024586; PubMed=3052286;
Gray W.R., Clivera B.W., Cruz b.C.;
"Poptide toxins from venomous Corus snails.";
Annu. Rev. Biochem. 57:665-700(1988).
-!- FUNCTION: Targets vasopressin-oxytocin related receptors.
-!- SUBCELLUAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.2%; Score 11; DB 1; Length 9; 25.0%; Pred. No. 1.3e+05; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              0; Indels
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
FMRFamide-like neuropeptide PF5 (AMRNALVRF-amide)
                                                                                                                                                          8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
                                                                                                                                                                                                                  26.2%; Score 11; DB 1; L
100.0%; Pred. No. 1.3e+05;
tive 0; Mismatches 0;
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01-NOV-1988 (Rel. 09, Last sequence update)
28-FEE-2003 (Rel. 41, Last annotation update)
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PROSITE; PS00264; NEUROHYPOPHYS_HCRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, B28495; B28495.
InterPro; IPR000981; Neurhyp_horm.
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S DLLEA 9
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                                                                                                                                                Katacka H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAL1 PICUA
P17440;
                                                                                                                                                                                                                                                                                                                                MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                  SEQUENCE
                                                                                                                                                                                                                 ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
TAL1 PICJA
                                                                                                                                                                                                                                Hua V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Calliphora vomitoria (Blue blowfly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, insecta; Pterygota;
Booptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Cestroidea;
Calliphoridae, Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                 (1) —
SEQUENCE, FUNCTION, AND AMIDATION.
MOÉTET C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
Matle A.G.,
"Isolation, characterization and pharmacology of FMRPamide-related
peptides (FARPS) from free-living nematode, Panagrellus redivivus.",
peptides (FARPS) from free-living nematode, Panagrellus redivivus.",
Submitted (JUL-2200) to the SWISS-PROT data bank.
-: FUNCTION: MYDACTIVE.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calliphora vomitoria.";
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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MEDLINE=92196111; PubMed=1549595;
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.; and activity of -Phe-Met-Arg-Phe-NH2
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                   i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11; DB 1; Length 9; Pred. No. 1.3e+05;
                                                                                                                                                                                                                             26.2%; Score 11; DB 1; Length 9; 33.3%; Pred. No. 1.3e+05; Live 3; Mismatches 1; Indels
Panagrellus redivivus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
CR S OR A.
29D00699CAB40457 CRC64;
                                                                                                                                                                                         MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last arnotation update)
CalliFMRFamide 10.
                                                                                                                                                                                                                                                                                                                                                                        9 A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%; 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Xatches 2; Conservative
                                                                                                                                                                                                                                           Best Local Similarity 33.3
Matches 2, Conservative
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                                                                                                                                                                              Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A44787; A44787
                                                                                                                                                                                                                                                                                 2 LRDDLL 7
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2 MRNALV 7
                                       NCBI_TaxID=6233
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ID PTSP BCMMO
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                                                                                                                                                                   FAMILY
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                               RESULT 10
FARA_CALVO
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P82003; 16-0CT-2001 (Rel. 4C, Created) 16-0CT-2001 (Rel. 4C, Last sequence update)

PA FI

STANDARD;

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"Identification of a prothoracicostatic peptide in the larval brain of the silkworm, Bombyx mori.";
the silkworm, Bombyx mori.";
5. Biol. Chem. 274:31169-31173(1999).
                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arch. Blochem. Blophys. 178:69-78(1977).

--- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF

METABOLITES IN THE FENTOSE-PHOSPHATE PATHWAY.

--- CATALYTIC ACTIVITY: Secondeptulose 7-phosphate + D-glyceraldehyde

3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.

--- FATHWAY: Pentose phosphate pathway, nonoxidative part.

--- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kataoka H.,
J. Biol. Chem. 275:9892-9892(2000).
-!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pichia jadinini (Yeast) (Candida unilish)
Pichia jadinini (Yeast) (Candida unilish)
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Nacilariales)
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Sun S.C., Joris L., Tsolas O.;
"Purification of crystallization of transaldolase isozyme I
evidence for different genetic origin of isozymes I and III
                                                                                                                                                                                                                                                                                                                                                                      STEAIN-C145 X N140, TISSUB-Brain,
MEDLINE-20002634, PubMed=10531308,
Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%; Score 11; DB 1; Length 9; 60.0%; Pred. No. 1.38+05; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -J., Tanaka Y., Nakamura K., Sakakibara M., Nagata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1008 MW; 274F31AF0E51E058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
3878C584472AB6C3 CRC64;
28-FEB-2003 (Rei. 41, Last annotation update)
Prothoracicostatic peptide (Bom-PTSP).
Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -.- ŠUBCEIJJLAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR
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InterPro; IPRC01585; Transaldolase.
PRCSITE; PS05958; TRANSALDOLASE 2; PARTIAL.
PRCSITE; PS01954; TRANSALDOLASE 1; PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRT;
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9 AA; 1C90 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chery Match
Best Local Similarity 60.03,
Best Local Similarity 60.03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Pentose shunt.
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                                                                                                                                                                                                          Bombycidae, Bombyx.
NCBI_TaxiD=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 A.
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SEQUENCE
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Eberly L., Crawford I.P.;

Suching The Treatment of Treatment o
                                                               Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D., Reinscheid R.K., Nothacker H.-P., Staley A.L.; "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-N#2 (Antho-RNamide), a garemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Protecbacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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PROSITE; PS50044; HTH LYSR FAMILY; FARTIAL.
Typtophan biosynthesis; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
64540729A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ci-JUN-1994 (Rel. 29, Created)
Ci-CJN-1994 (Rel. 29, Last sequence update)
01-F85-1995 (Rel. 31, Last annotation update)
TrpBA operon transcriptional activator (Fragment)
                                                                                                                                                                                                           U.S.A. 87:5410-5414(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 1; 1 Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                            L-3-PHENYLLACTYL.
                                                                                                                                                                                                     6 AA.
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              SEQUENCE, AND MASS SPECTROMETRY.
MEDLINE=90319122; PubMed=1973541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.8%;
Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             4 A.A.; 549 MW;
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Best Local Similarity 100.4
Thes 2; Conservative
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                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
MCD RES : 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRD 4
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NCN TER
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SEÇTENCE
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                                                                                                                                                                                 group."
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                                                                                                                                                                                                                                                                                                                                                                            01.MAR-1992 (Rel. 21, Created)
01.MAR-1992 (Rel. 21, Last sequence update)
01.CCT-1996 (Rel. 34, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (SC 6.2.1.19) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site for the lux operon.",

J. Bacteriol, 172:6802(1990)

-!- FUNCTION: ACYL-PROTEIN SYNTHETAGE ACTIVATES TETRADECANOIC ACID.

IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR COMPURFING TETRADECANOIC ACID. TO THE ALDERVIDE WHICH SERVES AS SUBSTRATE IN THE LUCFERASE-CAMPLYZED REACTION.

-!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91072226; PubMed=2254256;
Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: Bioluminescent fatty acid reduction system; second step
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antho-RNamide.
Anthopleura elegantissima (Sea anemone).
Bukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Actiniaria,
Nynantheae, Actinidae, Anthopleura.
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Vibrionaceae, Vibrio.
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Score 11; DB 1; LL.
Pred. No. 1.3e+05;
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                        3 A.A.
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Luminescence; Ligase.
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50.0%;
           Query Match
Best Local Similarity 50.0
Matches 2, Conservative
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Matches 1; Conserv
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Search completed: October 20, 2003, 13:46:19 Job time : 13 secs

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Q91bm8 simian viru Q99yX1 simian viru Q99yX1 simian viru Q99yX1 simian viru Q999X1 g-ycine max Q96m5 toxoplasma Q8ms1 bos taurus Q3592 saccharomyc Q8syj bacteriopha Q8hyj bacteriopha Q8hyi bacteriopha

Q9ps69 gallus gall Q98yk9 human immun Q8ayl5 carassius a

09PS69 098YK9 09BQT4 08AYL5

Q8H9H6 Q8H9H5 08H9H3 ALIGNMENTS

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(c) 1993 - 2003 Compugen Ltd.
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STRAIN&JRS4; Hogan D.A., DJ P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J., VarBogelen R.A.; "Two-dimensional gel electrophoresis map of Streptococcus pyogenes .. O Score 16; DB 2; Length 9; Pred. No. 8.3e+05; Bacteria, Firmicutes, Lactobacillales, Streptococcaceae; proteins."; Submitted (MAY-2000) to the SWISS-PROT data bank. -!- MASS SPECTROMETRY: NW=22592.04; METHOD=ELECTROSPRAY. 9 AA; 1369 MW; 2A771042CB1AB2D7 CRC64; 3; Mismatches SEQUENCE, AND MASS SPECTROMETRY. 38,1%; 40,0%; Conservative PRELIMINARY; Streptococcus pyogenes. Query Match Best Local Similarity Thes 2; Conserve DEVIE 8 B TITCE Streptccoccus. NCBI_TaxID=1314; SECTENCE P82568 P82568; RESULT 2 QBLPT5 RESULT 1 P82568 DETTO OCCUPANTA BENEFIT OCCUPA

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OBLPTS; C1-CCT-2002 (TrEMBLrel: 22, Created)

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SEQUENCE FROM N.A.
MEDLINE=97336048; PubNed=9192843; Ricewijk A.M., Hu.L., Schulz U., Tariveridan G., Hoeglund P., Ricer J., Ropers H.H., Kalscheuer V.M.; Moncallelle expression of human PEGI/MEST is paralleled by parent-specific methylation in fetuses."; Genomics 42:236-244(1997).
EMBL, Y15620; CAM71631.1, -. SEQUENCE 9 AA; 1258 MW; C52267340AB41412 CRC64;
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EMBL; AR125675; ARD22555.1; -. NON_IRA
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Cramata, Vertebrata, Euteleostomi;
Nammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxlD=9606;
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Best Local Similarity 66.7%; Pred. No. 6.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels
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Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
Hoogstraten D.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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NCBI_TaxID=90889;
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Best Local Similarity 40.04;
Thes 2; Conservative
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Bacteriophage phi-10.
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SEQUENCE
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MEDLINE=95255652; PubMed=7737502;

ASTULIAS J.D. DIAZ E., Timmis K.N.;

"Evolutionary relationship of the biphenyl dioxygenase of the grampositve bacterium Rhodococcus globerulus P6 to multicomponent dioxygenases of gram-negative bacteria.";

EMBL, X80041; CAA56350.1; -.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=cv. C123;
Ching A.S., Caidwell K.S., Jung M., Dolan M., Smith O.S., Tingey S., Ascapte M., Rafalski J.A.;
"SNP frequency, haplotype structure and linkage disequilibrium in elic maize inbred lines.";
Submitted (APR-2002) to the EMBL/GenBank/DDBC databases.
BMBL, AY094310; AMBLS6.1; -.
NON TER 1
SEQÜENCE 9 AA; 977 MW; 5CO5B2D2CB1AAAA3 CRC64;
                                                                                                                                     Eukarycta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Nocardiaceae, Rhodococcus.
NCBI_TaxID=33008;
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38.1%; Score 16; DB 10; Length 9;

Best Local Similarity 33.3%; Pred. No. 8.3e+05;

Antches 2; Conservative 4; Mismatches 0; Indels
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01-FEE-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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090826, 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
PEGI/MEST protein.
                        01-CCT-2002 (TrEMBLrel. 22, Last sequence update) 01-CCT-2002 (TrEMBLrel. 22, Last annotation update) Beta-expansin-like protein (Fragment).
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Best Local Similarity 33.3.
Best Local 2, Conservative
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Brinkman F.S.L., Francis F.W., Dillon J.R.;
Complexity the variable sequence between the carbamoyl-phosphate synthase genes of Neisseria species.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
BMB., AF029361; AAC7844911; -...
8 8
SEQUENCE 8 AA, 988 MW; FA372AB134032766 CRC64;
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Lawson F.S., Billowes F.M., Dillon C.A.;
"Organization of carbamcyl-phosphate synthase genes in Neisseria
gonorrhoeae includes a large, variable intergenic sequence which is
also present in other Neisseria species.";
Microbiology 141:0-0(0)
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Nelsseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Nelsseriales;
Nelsseriaceae; Nelsseria.
NCSI_TaxID=487;
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                                                                                                                                                                                                                                                                                                                       Query Match 33.3%; Score 14; DB 2; Length 8; Best Local Similarity 37.5%; Pred. No. 8.3e+35; Matches 3; Conservative 2; Mismatches 3; Indels
molecular methods.";
Submitted (JUN-2002) to the EMSL/GenBank/DDBJ databases.
EMBL: AY117046; AAM54119.1; -.
NON TER 8
SEQÜENCE 8 AA; 890 XM; F4D801A717111137 CPCEL.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
Carbamonyl-phosphate sylthase subunit 8 (Fragment).
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Q9ZIE9;
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.; O ö 99FS22; 01-MAR-200: (TEMBLrel. 16, Created) 01-MAR-200: (TEMBLrel. 16, Last sequence update) 01-MAR-200: (TEMBLrel. 16, Last sequence update) Hypothetical 1.0 kDa protein (Fragment). Clear arietinum (Chickpea) (Garbanzo). Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae; eurosids I: Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer. NCBI_TAXID=3827; SEQUENCE FROM N.A.

GOTSKI K., Rudng X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.,
"Dendrituc cell regulation of DCL1 mRNA expression.";
"Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF192526; AAF04643.1; -.
MGD; MGI:2136650; Dcll. Gaps Gaps Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus STRAIN=GV. Castellana, TISSUE=Etiolated epicotyl;
Dopico B., Cimenez T., Labrador E.;
"CDNA clones expressed in etiolated Cicer arietinum epicotyls.";
Submitted CEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ299(569; CACL0216.1;
Hypothetical protein. "Incompatibility repressor in a repA-like replicon of the IncFI plasmid Colv2-K94.";
C. Bacteriol. 166:1106-1112(1986).
EMBL: M13472; AAA23194.1; -. ; 0 .. O Query Match 33.3%; Score 14; DB 10; Length 9; Best Local Similarity 75.0%; Pred. No. 8.3e+05; Matches 3; Conservative 1; Mismatches 0; Indels 1; Indels Length 8; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) C-type lectin DCLI (Fragment) SEQUENCE 9 AA; 990 MW; 9441BDDAA7272EBE CRC64; 33.3%; Score 14; DB 2; 550.0%; Pred. No. 8.3e+05; tive 2; Mismatches 1; 9 AA. 9 AA. PRT; Query Match Sest Local Similarity 50.00. Best Local Similarity 50.00. PRELIMINARY; PRELIMINARY; Mus musculus (Mouse). | ':|: RIDILK 8 3 REDLIE 8 SECUENCE FROM N.A. NCBI_TaxID=10090; LLEA 9 NON TER SECTENCE φ Lectin. NON_TER C9DZA8 RESULT 10 RESULT 9 C90ZA8 ò SET RETERED SO SET RESERVED SO ò 5 40

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Sidnu M.S., Heir E., Sorum H., Holck A.L.;
Genetic linkage between quarernary ammonium compound and beta-lactam resistance in Staphylococci isolated from food.";
Submirted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYC28779; AAX38453.1;
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Marmalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_Tax1D=9606;
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                                                                                                                                                       01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-DEC-2001 (TYEMBLrel. 29, Last annotation update)
(Clone XP6A11A) (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Beta-lactamase repressor Bial (Fragment).
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SEÇÜENCE 8 AA; 930 MW; 4E3125B05AA44720 CRC64;
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Plasmid pST6.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Best Local Similarity 33.3
Matches 2, Conservative
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BMBL, AR443091, AAL34712.1; SEQUENCE 9 AA; 1102 MW; 1888D40B17272440 CRC64;
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MEDINE=8411508C: PubMed=6319754;
MEDINE=8411508C: PubMed=6319754;
MEDINE T.L., Hanafusa H.;
"Definer T.L., Hanafusa H.;
"DNA sequence of the Bryan high-titer strain of Rous sarcoma virus:
"DNA sequence of the Bryan high-titer strain of Rous sarcoma virus:
Extent of env deletion and possible genealogical relationship with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                            33.3%; Score 14; DB 11; Length 9; 75.0%; Pred. No. 8.3e+05;
                                                                                         1; Indels
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Rous sarcoma virus.
Viruses: Retrovid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=1:886;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. O., Created)
01-NOV-1996 (TrEMBLrel. O., Last sequence update)
01-NOV-1998 (TrEMBLrel. O8, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other viral strains.";
J. Virol. 49:549-556(1984).
BEL; K03365; AAA42557.1; -.
NON TER
SEQÜENCE 9 AA; 949 MW; 94AA144DDDD731AA CRC64;
  9 AA; 994 MW; 342161AB172EBAB7 CRC64;
                                                                                         0. Mismatches
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                     Query Match
Best Local Similarity 75.0%,
Best Local 3; Conservative
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Best Local Similarity 75.0'
Matches 3; Conservative
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Best Local Similarity 50.0
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STRAIN=00BW1471.27;
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VPJ.
  SQ SEQUENCE
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Q85710;
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Q85710
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RESULT 15

294DS4

AC Q9HDS4

CQHDS4,

CQHDS4,

CQHDS5,

COL-MAR-2001 (TEEMBLEE) 16, Last sequence update)

DT 01-MAR-2001 (TEEMBLEE) 16, Last annotation update)

CT-MAR-2001 (TEEMBLEE) 16, Last annotation update)

DE TrpC polyprotein (Fragment).

SASPETGILUS flavus.

CEUTATOR DOLYPROTEIN (Fragment).

CEUTATOR SOLON (Fragment).

CEUTATOR SOLON (Fragment).

CEUTATOR DOLTRATION (Fragment).

CEUTATOR (Fragment).
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Search completed: October 20, 2003, 13:48:25 Job time : 59 secs

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Peptide epitope of Peptide # 2 used i Rat Rb-interacting CXC zinc-finger b. Zinc finger protei Zinc finger protei Zinc finger protei Zinc finger mucleo Soluble peptide.

Human cancer-relat Human cancer-relat Human cancer-relat Human cancer-relat

AAU71211 ABR18988 ABR19174 ABR19426 ABR19578 ABR19780

AAW97373 AAB12035 AAU80810

ASG79371 ASP48411 ASP48414 ABP48419 Integrin alphaV-be Integrin alphaV-be ErbB2 cell overexp

ABP96179 AAW26557 AAB12069

AAB46568 AAB46668 AAB120938 AAB12096 AAB12096 AAA77888 ABB12498 ABB12556 ABB12554 ABB12554

Cel motif peptide
Ad40 cel peptide
Huma-2 restricted
Human G35 peptide

ABB12651 ABB12658 ABB12737 ABB12755

ABB12774 ABB12808

ABB12949

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WPI; 1999-142960/12
                                         23-JUL-1998;
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23-JUL-1997;
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Treel epicomper
Minor histocompati
Prenyl diphosphate
Human MHC molecule
Zifz68 zino finger
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HA-1 H-allele sequ
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                                                                                               October 20, 2003, 13:31:21 ; Search time 56 Seconds (without alignments) 25:510 Million cell updates/sec
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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Compugen Ltd
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            GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
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AAW99196
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AAW99195
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AAU71428
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

Intron, minor histocompatibility antigen HA-1; typing allele; H allele; R allele; Dolymorphic nucleotide; HA-1 typing; bone marrow transplant; severe aplastic anaemia; leukaemia; leukaemia; immune deficiency disease; ss. Ş AAW97374 standard; Protein; 9 98EP-0870125. 97EP-0202303. 98WO-EP04928 (first entry) (UYLE-) RICKSUNIV LEIDEN HA-1 R-allele sequence.

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Goulmy E;
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AAW97375
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                                                                                                                 antigen HA-1 R-allele. The specification describes methods for typing alleles (preferably the H and R alleles) of the minor histocompatibility antigen HA-1 in a sample, which comprise detecting polymorphic nucleotides in the cDNA or genomic nucleic acids of the alleles. The methods can be used for HA-1 typing for bone marrow transplants, severe aplastic anaemia, leukaemia and immune deficiency diseases, as well as detection of genetic aberrances. The probes and primers of the invention can be used to screen for the HA-1 alleles. The HA-1 peptides can be used anti-idiotypic B cells and/or T cells and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a new peptide (F1) constituting a T-cell epitope cheainable from the minor histocompatibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. Pi is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anaemia; immune deficiency disease.
                                                                                                     present sequence represents part of the minor histocompatibility
                                                                                                                                                                                                                                                                                                                                                                Gaps
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Typing minor histocompatibility antigen HA-1 - by amplifying and identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection of genetic aberrances
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99197 standard; peptide; 9 AA
                                                                     Claim 13; Fig 5; 59pp; English.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLRDDLLEA
                                                                                                                                                                                                                                                                                                9 AA;
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                                                100.0%; Score 42; DS 20; 100.0%; Pred. No. 9.3e+05;
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Sest Local Similarity
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9 AA;
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RESULT 4

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(UYLE-) RIJKSUNIV LEIDEN.
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                                                                                                                                                         Minor histocompatibility antigen, HA-1, T-cell epitope, immunological, graft versus host disease, bone marrow transplant, leukaemia, vaccine, diagnosis, aplastic anaemia, immune deficiency disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new minor histocompatibility antigen, HA-1 - useful to treat
immune diseases and prevent rejection and host versus graft disease
in bone marrow and organ transplantation
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Pred. No. 9.38+05;
Transtrhes 1; Indels
                                                                                                                   Minor histocompatibility antigen HA-1 T-cell epitope #2
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  AAW99196 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goulmy EacM,
                                                                                                                                                                                                                                                                                                                                                                                                     97EP-0202303
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                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           UYLE-) RICKSUNIV LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VLRDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-153312/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                               WO9905174-A1
                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1997;
                                                                             20-MAY-1999
                                                                                                                                                                                                                                                                                                                       04-FEB-1999
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                                                                                                                                                           Minor
graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
AAW97572
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The present sequence represents an immunogenic peptide constituting a T-cell epitope, obtainable from the minor histocompatibility antigen HA-1. The peptide can be used in vaccines or pharmaceutical formulations as medicines to induce telerance for transplants so as to prevent sejection and/or Graft-versus-Host Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells presenting the peptides, in an HLA class I context, can be eliminated after specific recognition of the peptides. The peptides can also be used to raise antibodies, T-cell receptor, b- and T-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anaemia; immune deficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                              immunogenic peptide from minor histocompatibility antigen HA-1 -
useful for inducing tolerance to transplants and prevent rejection
or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 36; DB 20; Length 9; 88.9%; Pred. No. 9.3e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minor histocompatibility antigen HA-1 T-ceil epitope #1.
                                                                                                                                                                                                                     Hunt DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99195 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1: Page 39; 57pp; English.
                                                                                                                                                                                                                     Goulmy EAJM,
98WO-NL00424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-NL00425
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                                                                                                                                        (LYLE-) RIJKSUNIV LEIDEN
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Sequences AAUT1093-AAUT1796 represent the 1019728-related protein and peptide fragments of the protein. 103P328 exhibits tissue specific many cancers including timburs of the prostate, but it is also aberrantly expressed in many cancers including timburs of the prostate, bladder, kidrey, colon, lung, breast, rectum and stomach. The 103P3E8 polynucleotide, its related useful for diagnosing and stomach. The 103P3E8 polynucleotide, its related polynucleotide which encodes a single chain monoclonal antibody, that chaminospecifically binds to an 103P3E8 related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P3E8 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P3E8. The sequences can be used in diagnostic methods to monitor the level of 103P3E8 gene products in serum, blood, urine and tissue and to thereby detect the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                        1039328; prostate; bladder; kidney; colon; lung; breast; rectum; stomach; tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme; single chain monoclonal antibody; serum; blood; urine; tissue; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring 103P3E8 gene products in sample from patient (suspected of) having cancer, useful for diagnosing, managing or treating cancers, e.g. prostate cancer, comprises determining presence of aberrant 103P3E8 gene products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Afar DEH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                     Score 27; DB 19; Length 9;
Pred, No. 9.3e+C5;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Human MHC molecule HLA-All binding 103P3E8 peptide #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitchell SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.5%; Score 25; DB 23;
llarity 62.5%; Pred. No. 9.3e+05;
Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 90; 128pp; English.
                                                                                                                                                                                                                                                                          AAU71428 standard; Pertide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (URGG-) UROGENESYS INC.
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Best Local Similarity
Thes 5, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 9q13-q21
                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                          2 LRODILE 8
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                                                                                                                                                    : ||::
9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WC200179557-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Faris M, Cha
Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                           26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2001
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                                                                                                                                                                                                                                                                                                                  AAU71428;
  Sequence
                                                                                                                                                                                                                               RESULT 8
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                                                                                                                                                                                                         The present sequence represents a new peptide (PI) constituting a T-ceil epitope obtainable from the minor histocomparibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. Pi is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence from preserved region VI of prenyl diphosphate synthetase (PDS), was used in the preparation of primers for the amplification of PDS DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Substances synthesised by PDS, i.e. polyprenyl diphosphates, are precursors of physiologically active substances, e.g. vitamin K and ubiquinones.
                                                                                A new minor histocomparibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prenyl diphosphate synthetase; polyprenyl diphosphate, vitamin K_{\rm r} ubiquinone; preserved region VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding prenyl diphosphate synthetase subunit(s) - new
Micrococcus prenyl diphosphate synthetase subunit polypeptide(s)
and methods for preparing enzymes from subunit(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 20; Length 9;
Pred. No. 9.3e+05;
0; Mismarches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogura K;
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    댰.
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    Hunt
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                                                                                                                                                                        Claim 1; Page 32; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%;
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    Goulmy EAJM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : VLRDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Thes 8; Conserve
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                                             WPI; 1999-153312/13.
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                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
    Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-1997;
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Shimizu N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW47427;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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AAU71211 standard; Peptide; 9

AAU71211;

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The present sequence is a randomised DNA-binding domain on the alpha-helix of a zinc finger of the transcription factor zifz68. It was alpha-helix of a zinc finger of the transcription factor zifz68. It was concreted in an example to illustrate an invention relating to a library of DNA sequences; where N is at least 3. Each sequence has one of the 4N sequences, where N is at least 3. Each sequence has one of the 4N sequences of a DNA sequence of length N. The library is useful for designing a zinc finger polypeptide having specificity for a particular DNA sequence. Typically a zinc finger motif is designed, produced by recombinant or synthetic methods and ontacted with an immobilised DNA library. Briding is detected and the specificity and affinity of the zinc finger protein may be modified to increas in the specificity and affinity. The library is also useful for determining the preferred base recognition specificity of zinc finger proteins. The designed zinc finger proteins are useful for therapy, e.g. targeting mutations in targeting double stranded DNA, for diagnosis, e.g. detecting mutations in gene sequences, and for DNA purification.
                                                                                                                                                                               Human immunodeficiency virus type 1, HIV-1, zinc finger protein; 21f268;
DNA library; DNA chip; DNA binding domain; therapy; mutation detection;
DNA purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library of DNA sequences immobilized on a solid support for selecting and designing polypeptides, comprising nucleic acid binding motifs, in particular zinc finger polypeptides.
                                                                                                                                                 Zif268 zinc finger alpha-helix randomised DNA-binding domain #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24, DB 22; Length 7; Pred. No. 9.3e-05; 1; Indels 0; Mismatches 1; Indels
                                    AAB81550 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 2; 43pp; English
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30-MAY-2000; 2000GB-0013106
                                                                                                                                                                                                                                                                                                                                                                                       02-CCT-20CG; 2000WO-GBC3765
                                                                                                               (first entry)
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Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-266303/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klug A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA;
                                                                                                                                                                                                                                                                                                          W0200125417-A2.
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                                                                                                               18-JJN-2001
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                                                                                                                                                                                                                                                                    Synthetic
                                                                          AAB81550;
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                  AAB81550
RESULT
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                                                                                                                                 stomach;
                                                                                                                              103F9BB; prostate; bladder; kidney; colon; lung; breast; rectum; stom:
tumcur; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
single chain monocional antibody; serum; blood; urine; tissue; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring 103F3B9 gene products in sample from patient (suspected whaving carcer, useful for diagnosing, managing or treating cancers, e.g. prostate cancer, comprises determining presence of aberrant 103P3E8 gene products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                Human MHC class I molecule HLA-A2 binding 103P3E8 peptide #18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer-related protein 184P3G10 Hih peptide #223.
                                                                                                                                                                                                                                                                                                                                                                                                                     Raitano AB, Mitchell SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 23; T Pred. No. 9.3e+05; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 84; 128pp; English.
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100.0%; Pre/
0; F
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                                                                                                                                                                                                                                                                                                                    12-APR-2001; 2001WO-US12181
                                                                                                                                                                                                                                                                                                                                                      12-APR-2000; 2000US-196647P
                                                                                                                                                                                                                                                                                                                                                                                                                        Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (UROG-) UROGENESYS INC
                                                                                                                                                                                  chromosome 9q13-q21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-061976/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                  WC230179557-A2
                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       Faris M, Cha
Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-2003
                                                                  26-FEB-2302
                                                                                                                                                                                                                                                                                   25-OCT-2501.
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The present invention relates to novel human cancer-related genes and proteins (AB27912C-AB279168 and ABR01789-ABR01661). The genes and proteins are useful for eliciting a humanal or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the adjagnosis and/or prognosis of cancer, as coding sequence capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                                                                                                                                                                                                             New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response
             Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%; Score 23; DB 24; Length 9; 71.4%; Pred. No. 9.3e+05; 1.0els 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen:
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                                                                                                                                                                                                                                                                                  Ge ¥,
                                                                                                                                                                                                                                                                                  Faris M,
                                                                                                                                                                                                                                                                         Vakobovits A, Chalitta-μιν τ...,
νατηγορι Κ, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13, Page 306, 1021pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR19174 standard; Peptide; 9 AA
                                                                                                                                                                                   10-APR-2001; 2001US-282739P.
10-APR-2001; 2001US-283112P.
25-APR-2001; 2001US-286630P.
                                                                                                                                                       1C-APR-2002; 2002WO-USI1654
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                WPI; 2003-075555/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
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                                                                                                                         24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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ABR19174
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Hubert RS;

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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABX01789-ABR01861). The genes and proteins are useful for alloiting a humoral or callular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, manAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic prognostic and diagnostic reagents for cancer. The present sequence is a numan leukocyte antigen (MLA) peptide, used in an example from the invention.
                                                                                                                                                                                   New composition comprising a substance that modulates the structure of
proteins and polynuclectides, useful for therapeutic, prognostic and
diagnostic reagents for eliciting cellular or humoral immune response
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                                                                                                                  Hubert RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 24; Length y; Pred, No. 9.3e+05; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytostatic; vaccine; cancer; immune response; HLA;
human: leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer-related protein 18423G10 HLA peptide #661.
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se:
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                                                                                                                  Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jakobovits A, Challita-Eid PM, Faris Morrison K, Morrison RK, Raitano AB;
                                                                                                            Jakobovits A, Chalitta-muse, ...
Morrison K, Morrison KK, Raitano AB,
                                                                                                                                                                                                                                                            Claim 13; Page 308; 1021pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR19426 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%;
71.4%;
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10-APR-2001; 2001US-283112P.
25-APR-2001; 2001US-286630P.
                         10-APR-2001, 2001US-282739P.
10-APR-2001, 2001US-283112P.
25-APR-2001, 2001US-28663CP.
10-APR-2002; 2002WO-US11654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-APR-2002; 2002WO-US11654
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                                                                                                                                                         WPI; 2003-075555/07.
                                                                                                                                                                                                                                 cancer patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
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ABR19426
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Homo saptens 19-MAY-2003 24-CCT-2002. Jakobovits Morrison K, Sequence ABR19578; RESULT 14 ABR19578 CD.

New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response

WPI; 2003-075555/07.

Claim 13; Page 313; 1021pp; English

cancer patients

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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78160 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or callular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proceins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present
The present invention relates to novel human cancer-related genes and proteins (ABZ70120-ABZ70168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humaner of cellular immune response. The genes are useful as probes and primers for the amplification and/or diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as the responsition and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                                                                                                                                                                                                                                                                                                                                    Score 23; DB 24; Length 9;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, cytostatic, vaccine, cancer, immune response, HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cancer-related protein 184P3G10 HLA peptide #1015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jakobovits A, Challita-Eid PM, Faris
Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 315; 1021pp; English.
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                                                                                                                                                                                                                                                                                                                                54.8%;
71.4%;
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10-APR-2001, 2001US-283112P.
25-APR-2001, 2001US-286630P.
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ABR19780
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                                                                                                                                                                                                                    The present invention relates to novel human cancer-related genes and proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humonal or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the adjaponsis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic and diagnostic research for cancer. The prosest therapeutic and diagnostic research for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                                                                  New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response
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Pred. No. 9.3e+05;
L. Mismatches 1; Indels
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Raitano AB;
                                                                                                                                                                                Claim 13; Page 311; 1021pp; English
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10-APR-2001; 2001US-283112P.
25-APR-2001; 2001US-286630F.
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Morrison RK, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-2002; 2002WO-US11654
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Best Local Similarity
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                         WPI; 2003-075555/07
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                                                                                                                                         cancer patients
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CC sequence is a human leukocyte antigen (HLA) peptide, used in an example CC from the invention.
X Sequence 9 AA;
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                                                                                                                                Query Match 54.8%; Score 23; DB 24; Length 9; Best Local Similarity 71.4%; Pred. No. 9.3e+05; Matches 5; Conservative 1; Mismatches 1; Indels
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Search completed: October 20, 2003, 13:45:48 Job time : 57 secs

2 LRDDLLE 8 :: | | | | 2 LRGELLE 8

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Sequence 16, Apple Sequence 116, Apple Sequence 228, Apple Sequence 211, Apple Sequence 216, Apple Sequence 211, Apple Sequence 216, Apple 2
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                                                                                                                                                     October 20, 2003, 13:48:32 ; Search time 43 Seconds (without alignments) 34.308 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-990-186-21
US-09-991-186-218
US-09-989-994-218
US-09-989-994-216
US-09-989-994-216
US-10-166-225A-168
US-10-166-225A-169
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US-09-834-765-132
US-09-989-789-208
US-09-989-789-211
US-09-989-789-211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                609560 segs, 163917102 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length DB
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Maximum DB seq length: 9
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                Rur on:
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Seguence 170,		a)		a)	-	Sequence 20,	equence 2	22	e :2	07.0	34	ű	4	62	295	equence 3	equence 39	e 39	equence 3	39	equence 39	Sequence 29	'n	m	equence 3	m	Seguence 39	Seguence 39	Sequence 29
.10-166-225A-17	0-Tep-0	-10-166-225A-17	10-166-2	US-10-271-708-8	-801-784-	9-801-784-2	-09-801-784-2	- 78	-09-932-165-12	-09-935-384-1	US-09-935-384-349	-09-935-384-51	-09-935-384-54	-09-935-3	39-989-789-295	19-989-78	19-989-189-391	39-989-789-39	19-989-789-391	39-989-789-393	19-989-189-394	-09-990-186-2	-09-990-186-38	-990-186-39	-09-990-186-39	-09-990-186-391	-09-990-186-39	-990-186-394	-989-994-295
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FILE REFERENCE: 129, 61501.

FILE REFERENCE: 2001-03-21.

PRICE APPLICATION NUMBER: 60/197,647.

PRICE APPLICATION NUMBER: 60/197,647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.5%; Score 25; DB 9; Length 9; 62.5%; Pred. No. 5.46+05; ive 2; Mismatches 1; Indels
Sequence 349, Application US/39834765
Patent No. US20220055478A1
GENERAL INFORMATION:
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Best Local Similarity 62.5.
The 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-09-834-765-349
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RESULT 2 US-10-271-768-16 ; Sequence 16, Application US/10271708

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US-09-589-789-21.
Sequence 211. Application US/69989769
Federic 0. US202053379A.
General INCORMITION
GENERAL INCORMITION
TITLE CF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE CF INVENTION: POSITION DEPENDENT FINGERS
TITLE CF INVENTION UNDER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 216, Application US/09989789

Patent No. US20020053379A1

GENERAL INFORMATION:

APPLICANT: LIU Qiang

TILLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF ONN NUCLECTIDE

TILLE OF INVENTION: TAPPLETS BY ZINC FINGERS

FILLE REFREAMENDES: 8125-0311.25

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ LD NOS: 4085

SOFTWARE: Patentin Ver. 2.0

LENGTH: 7
                                                                                                                                                                                                                                    . CTRER INFORMACION: Description of Artificial Sequence: example ZFP US-09-989-789-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-29-989-783-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Score 21; DB 9; Length 7; 66.7%; Pred. No. 5.4e+05; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                     Query Match 50.3%; Score 21; DB 9; Length 7; Best Local Similarity 66.7%; Prod. No. 5.4e+05; Matches 4; Conservative 1; Mismatches 1; Indels
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT PAPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SCFTWARE: ParentIn Ver. 2.0
SEC ID NO 208
LENGTH: 7
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                           CRGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 66.7
Matches 4, Conservative
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                                                                                                                                                                            TYPE: PRT
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Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
                                           APPLICANT: CHOO, Yen
APPLICANT: CHOO, Yen
APPLICANT: LIU, Xiaohai
APPLICANT: BLASUBRAMANIAN, Shankar
APPLICANT: BALANUBRAMANIAN, Shankar
APPLICANT: ISALAN, Mark
TITLE OF INVENTION: METHODS FCR MODULATING TELOMERASE ACTIVITY
FILE REPERENCE: SABI-036/01US (8125-2014.01)
CURRENT APPLICATION NUMBER: US/10/271,708
CURRENT FILING DATE: 2cc2-10-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Fatentin version 3.2
SEQ ID NO 16
LENGTH: 7
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Parent No. US200200547841
GREERL INFORMATION:
GREERL INFORMATION:
APPLICANT: Mary Faria
APPLICANT: Pla M. Challita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Aya Cakobovits
TITLE CF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE CF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE CF INVENTION: AND DETECTION OF CANCER
FILE REFERENCE: 129:6USU
CURRENT APPLICATION NUMBER: US/09/834,765
CURRENT FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 77C
SEC ID NOS: 77C
SEC ID NO 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 12; Length 7;
Pred. No. 5.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%; Scor
83.3%; Pred
0;
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT .
CRGANISM: artificial sequence
  Publication No. US20030162200A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ) CTHER INFORMATION: F2 residue US-10-271-708-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.1
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 5, Conservative
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CRGANISM: Homo sapiens
US-09-834-765-132
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US-09-989-789-208
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Gaps

) Offick INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-216

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Gaps

Query Match

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US-09-989-994-21:
| Sequence 211, Application US/09989994 |
| Publication No. US2030104526A; |
| Publication No. US2030104526A; |
| GENERAL INFORMATION: |
| APPLICANT: LIU, Qiang |
| TILLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE |
| TILLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE |
| TILLE OF INVENTION: RIPLETS BY ZINC FINGERS |
| FILE REPERENCE: 8325-0011.20 / S11-US2 |
| CCRRENT APPLICATION NUMBER: US/09/989,994 |
| CCRRENT FILING DATE: 2001-11-20 |
| NUMBER OF SEQ ID NCS: 4065 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO. 211 |
| ENGINE OF 211 |
| ENGINE OF 212 |
| ENGINE OF 212 |
| ENGINE OF 213 |
| ENGINE OF 214 |
| ENGINE OF 215 |
| ENGI
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Publication No. US20300164526A1
GENERAL INFORMATION:
APPLICANT: LIU, Clarg
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY 21NY FINGERS
TITLE OF INVENTION: TRIPLETS BY 21NY FINGERS
FILE REFERENCE: 8325-0611.20 / S1-US2
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 208
                                   APPLICANT: LIJ, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS SYZINC FINGERS
TITLE CF INVENTION: TRIPLETS SYZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11.20
NUMBER OF SEQ ID NOS: 4685
SOFTWARE: PATENTIAN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: example ZFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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66.7%;
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ORGANISM: Artificial Seguence
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Best Local Similarity 66.00
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Best Local Similarity 66.,
4, Conservative
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US-09-989-994-208
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                     Sequence 208, Application US/09990186
Publication No. US20030668675A1
GENERAL INFORMATION:
APPLICANT: LIU, Olang
TITLE OF INVENTION: POSITION DEPENDENT RECCGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY INFO FINGERS
FILE REFERENCE: 8325-C011.21 / S11-US3
CURRENT FILING DATE: 2061-11-20
NUMBER OF SEC ID NOS: 4085
SOFTWARE: PATENTIN VOR: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 211, Application US/0990186
Publication No. US20030068675A1
APPLADAL INFORMATION:
APPLICAMT: LIU, QIANG
TITLE OF INVENTION: PCSITION DEPENDENT RECCGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENDE: 8125-601.12 / $11-US3
CURRENT PILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: example 2FF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 21; DB 11; Length 7; 66.7%; Pred. No. 5.4e+05;
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   Score 21; DB 9; Length 7; Pred. No. 5.4e+05;
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US-09-990-186-216
; Sequence 216, Application US/09990186
; Publication No. US2C030068675A1
50.0%;
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ORGANISM: Artificial Sequence
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Matches 4, Conservative
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Query Match

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FEATURE:

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RESULT 14
US-10-166-228-163
US-10-166-228A-163
Sequence 168, Application US/ICI66225A
Publication No. US2C0301434;6A1
GENERAL INFORMATICN:
APPLICANT: BEREY, Alan
APPLICANT: BRETZEL, Wetner
APPLICANT: BRETZEL, Wetner
APPLICANT: LOPEZ-JULBARRI, Rual
APPLICANT: MYRELIN, Warkus
APPLICANT: MYRELIN, Warkus
APPLICANT: WHINESTIN, Rual
APPLICANT: WELLISE V. Alexei A.
ITLE OF INVENTION: INPROVED ISOPRENOID PRODUCTION
ITLE OF INVENTION: INPROVED ISOPRENOID
ITLE OF INVENTION: UNPRES: US/10/166,225A
CURRENT FILLS OF 202.06-05
NUMBER OF SEQ ID NOS: 197
SEQ ID NO 168
LENDIAL:
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Best Local Similarity 60.0%;
Matches 3; Conservative 5
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Matches 3; Conservative
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Sequence 216, Application US/0989994
Publication No. US20033104526A1
CENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECCGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: POSITION DEPENDENT RECCGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: PIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PALENTIN Ver. 2.0
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example 2FP
US-09-989-994-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-985-994-216
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                                                                                                                                            Query Match 50.0%; Score 21; DB 11; Length 7; Best Local Similarity 66.7%; Pred. No. 5.4e+05; Matches 4; Conservative 1; Mismatches 1; Indels
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Sequence 54, Application US/09833203
Sequence 54, Application US/09833203
PUBLication No. US20030:66277A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ennest S.
ATTLE ON INVENTY ON TAYGETED Vaccine Delivery Systems
FILE REPERBUCE: 1821.0020061
CURRENT APPLICATION NUMBER: US/09/833,203
CURRENT APPLICATION NUMBER: US/09/833,203
CURRENT APPLICATION NUMBER: US/09/833,203
FRICE FILING DATE: 2001-04-12
PRICE FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
SEQ ID NO 54
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; OTHER INFORMATION: C35 peptides
US-09-833-203-54
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 4, Conservative
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ô ö Gaps Gaps ., 47.6%; Score 20; DB 12; Length 5; 60.0%; Pred. No. 5.4e+65; Length 5; 0; Inders 0; Indels APPLICANT: BERRY, Alan
APPLICANT: BERRY, Alan
APPLICANT: BERTZEL, Werner
APPLICANT: BERTZEL, Werner
APPLICANT: BUYBELIN, Markus
APPLICANT: MAYER, Anne F.
APPLICANT: MAYER, Anne F.
APPLICANT: WEISEV, Alexei A.
TILL OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REFERENCE: C18435/12196
CURRENT: APPLICATION NUMBER: 35/10/166,225A
CURRENT: FILING DATE: 2022-06-05
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 169 Score 20; DB 12; Fred. No. 5.4e+05; 2; Mismatches 0 2; Mismatches Search completed: October 20, 2003, 14:01:22 TYPE: PRT ; ORGANISM: Rhizobium sp. strain NGR234 US-10-166-225A-169 Sequence 169, Application US/10166225A Publication No. US20030148416AL GENERAL INFORMATION: ORGANISM: Bradyrhizobium japonicum

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                                                                                                     October 20, 2003, 13:43:56 ; Search time 20 Seconds (without alignments) 19.040 Million cell updates/sec
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Sequence 14,
Sequence 26,
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US-08-873-235B-11
US-08-873-235B-11
US-08-156-8-20
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US-09-586-472-20
US-09-586-472-20
US-09-586-475-20
US-08-459-411-75
US-08-5199-411-75
US-08-519-8-75-75
US-09-528-70-75
US-08-516-859A-75
US-08-516-859A-72
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000000000	1.1-609A- mnce 11,7-609A- mnce 11,7-609A- ERAL INFO FELICANT: FELI	PCLOGY: li PCLOGY: li CULE TYPE: -609A-11 atch cal Similari
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	RESULT : US-09-21'-6094-11 Sequence 1: Application US/392176599 Fatent No. 6571733 GENERAL INFORMATION: APPLICANT: WOURE, Ayum: APPLICANT: SHINIZJ, Nacto APPLICANT: GENERALS. INVERE OF SEQUENCES: 29 CORRESPONDENCES: 29 CORRESPONDENCES: 29 CONNERS: 1025 Connecticut Avenue STREET: 1025 Connecticut Avenue CITY: Washington STREET: 1025 Connecticut Avenue CONNERS: BEADABLE FORM: XEDIUM TYPE: 3.5 inch Floppy di CONNERS: 203-6 CONNERS: 203-6 CONNERS: 203-6 CONNERS: APPLICATION DATA: APPLICATION NUMBER: US/C9/217,6 FILING DATE: 11-Un-1997 ATIONEY/AGNT: INFORMATION: NAME: TOFFENDENT! APPLICATION NUMBER: 39.048 REFERENCE/DOCKET NUMBER: 39.048 REFER	JS-C Ma
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US-08-459-568-20
Sequence 20, Application US/08459568
Parent No. 5813304
GENERAL INFORMATION:
APPLICANT: Huang, Sh:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 21; DB 2; Length 6; 80.0%; Pred. No. 2.5e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0%; Pred. No. 2.5e.05;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

CEDIUM TYPE: Floppy disk

CEDIUM TYPE: Floppy disk

CENSURAR: Per Compatible

OPERATING SYSTEM: PC-DOS/MS-DCS

SOFWARE: Parentin Release #1.C, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,568

FLING DATE: 02-UN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/399,411

FLING DATE: 06-MAR.1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,315

REGISTRATION NUMBER: 31,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 730
CITY: San Diego
STATE: California
APPLICANT: Snyder, Sclomon TITLE OF INVENTION: Huntingtin-associated protein FILE REFERENCE: 01107.5227. CURRENT APPLICATION NUMBER: US/08/556,419C CURRENT FILING DATE: 1995.11-09 NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID 01.4 LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619; 518-8949; INFORMATION POR SEQ 1E NO: 20; SEQUENCE CHARACTERISTICS; ENGYE: 6 amino acids
                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuery Match
Sest Local Similarity 80.0
Matches 4, Conservative
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// TOPCLOGY: linear
US-08-459-568-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               # BOLLCO #
                                                                                                                                                                                                                                                                                                                                                                                                                            4 DOLLE 8
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                                                                                                                                                                                                                                                                             JS-08-556-419-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
                                                                                                                                                                                                                                                           APPLICANT: WITHAMATSU, Masayoshi
APPLICANT: KOIKE, Ayumi
APPLICANT: KOIKA, Kyozo
APPLICANT: KOURA, Tanetcoshi
APPLICANT: KOYMA, Tanetcoshi
APPLICANT: SHIMIZU, Naoto
APPLICANT: CHO, Yenwin
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
NUXAER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.3%; Score 27; DB 3; Length 9; 57.1%; Pred. No. 2.5e+05; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, NW - Suite 600
CITY: Waghington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
CITY: Washington
COUNTRY: US
ZIP: 20036
COMPUTER BADABLE FORM:
MEDIUM TYPE: 3.5 inch Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WORDPEFECT 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,235B
FILING DATE: 1.-Jun-1997
CLASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: JP 154441/1996
ATTOREY/AGANT INFORMATION:
NAME: TOFFENETT: Judith L.
REGISTRATION NUMBER: 39,048
REGISTRATION NUMBER: 39,048
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-556-419-14
Squence 14, Application US/08556419C
Patent No. 6093549
GENERAL INFORMATION:
APPLICANT: Ross, Christopher
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Shi-Hua
APPLICANT: Li, Shi-Hua
APPLICANT: Sharb, Alan
APPLICANT: Marlan, Anthony
APPLICANT: Worley, Paul
                                                                                                                                                                                                Sequence 11, Application US/08873235B Patent No. 6174715
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1
Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MCLECULE TYPE: peptide
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                                 2 LRODLLE 8
                                                          3 IRCOILD 9
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FRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/399,411

FILING DATE: 06-WAR-1995

FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683

FILING DATE: 18-M30-1994

ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNMBER: 31,815

REGISTRATION UNMBER: P-LJ 1776

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 515-9901

TELEPHONE: (619) 515-9901

TELEPROME GIARAFICE: 05001

TELEPAK: (619) 515-9901

TELEPAK: (619) 515-9901

TELEPAK: (619) 515-9901

TELEPAK: (619) 515-9901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09596472; Patent No. 6233333
GENERAL INFORMATION:
APPLICANT: Huang, Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535-8949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 DDTLE 8
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Sequence 20, Application US/08516859A
Sequence 20, Application US/08516859A
Sequence 20, Application US/08516859A
Sequence 20, Application US/08516859A
Sequence 20, Application US/0851685A
TITLE OF INVENTION:
TO CORRESPONDENCES:
                              US-08-399-411-20;
Sequence 20, Application US/08399411;
Patent No. 5831008;
GENERAL INFORMATION:
TITLE OF INVENTION:
TORRESPONDENCE:

MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CALLIOFICIA
COUNTRY: USA
ZIP: 92122
COMPUTER READARE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC COMPATIBLE
OFFRALICS OFFRALICE: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 53
ATTORNEY/ACBNT INFORMATION:
NAME: Campbell, Cathyn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9901
INFORMATION FOR SEQ ID NO: 2C:
SEQUENCE CRARACTERISTICS:
LENGTH: 6 amino acids
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MEDILY TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/516,859A
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell & Flores LDF
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 21; DB 2; 1
60.0%; Pred. No. 2.5e+05;
tive 1; Mismatches 0
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Best Local Similarity 60.0
Matches 4; Conservative
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CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 DDLLE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-399-411-20
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Gaps
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NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
Score 21; DB 3; Length 6; Pred. No. 2.5e+05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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Patent No. 5871038
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TTLE OF INVENTION: Retinoblastoma Protein - Interacting
TTLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE AND CORRESPONDENCE AND LA GOLD AND LA
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADRESSE: Campbell and Flores
STREET: 4370 La Joha Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 21; DB 2; Length 8; 80.0%; Pred. No. 2.5e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

REDICK TYPE | Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: F2-DOS/MS-DCS

SCETWARE: Patentin Release #1.0, Version #1.25

CURRENTED: Patentin Release #1.0, Version #1.25

CURRENTED: DATE: US/08/459.569

FILING DATE: US/08/459.569

FILING DATE: US/08/459.569

FILING DATE: US/08/459.569

FILING DATE: US/08/459.569

FROM AGENT INCORMER: US/08/399,411

FILING DATE: US/08/399,411

FILING
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COMPUTER: 1BX PC COMPATIBLE
COPRATING SYSTEM: PC-DCS/NS-DOS
SOFTWARE: Patertin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/CA/399,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-MAR-1995
CLEASSFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 75, Application US/08399411
Patent No. 5831008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTCRNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 8 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPCLOGY: linear
US-08-459-568-75
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Patent No. 6463985
GENERAL INFORMATION:
APPLICANT HUBBY
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Ficres LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                          50.0%; Score 21; DB 4; Length 6; 80.0%; Pred, No. 2.5e+05;
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MEDIUM TYPE: Floppy disk
COMPUTER: PER PLOPPY disk
COMPUTER: PREST POSPY PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/528,706
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Pred. No. 2.5e+05;
1; Mismatches 0
                                                                                                                                                                                                                                                                                              1; Mismatches
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FRICHS DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-40G-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (6.9) 535-8949
INFORMATION FOR SEG ID NO: 20:
SEQUENCE CHARACTERISTICS:
    TYPE: amino acid
TCPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 75, Application US/08459568 Patent No. 5811304 GENERAL INFORMATION:
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENGTH: 6 amino acid
TYPE: amino acid
TOPCLOGY: linear
US-09-528-706-20
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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| EDLLE 5
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Patent No. 5872210
SENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ALDRESS:
ADDRESSEE: MOREAN & FINNEGAN, L.L.P.
CORRESPENCE AND AND ADDRESSEE: MOREAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: FLOPPY DISK
COMPUTER: FLOPPY DISK
COMPUTER: PCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,432
FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
RECISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 36,434
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4801
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                REFERENCE/DOCKST NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                      50.0%;
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Best Local Similarity 80.09
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Best Local Similarity 80.0
Lac 4; Conservative
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TOPOLOGY: Linear
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                                                                                                                                                              TYPE: amino acid
TOPCLOGY: linear
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                                                                                                                                                                                                                                                                                                                     4 DDLLE 8
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                                                                                                                                                                                                 US-08-399-411-75
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US-09-586-472-75
US-09-586-472-75
Sequence 75, Application US/39586472
Sequence 75, Application US/39586472
GENERAL INFORMATION:
PAPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
Patent No. 6669211
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NIYBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                CUNTRY: USA

COUNTRY: USA

CONPUTER: EN PC COMPATABLE
COMPUTER: ISM PC COMPATABLE
COMPATER: PATENTIN PELSES
CONFORTER: PATENTIN PELSES
CONFORTER: USA

CONFORTER: USA

CONFORTER: USA

SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/06/516,859A

FILING DATE: 18-AUG.1995

CLASSIFICATION NUMBER: US/06/516,859A

FILING CATE: 06-WAR-1995

FILING CATE: 06-WAR-1995

FILING CATE: 06-WAR-1995

FILING CATE: 18-AUG.1994

APPLICATION NUMBER: US/08/516,839

FILING CATE: US-WAR-1995

REGISTRATION NUMBER: US/08/516,839

FILING CAMPELIA CATHYN A.

REGISTRATION NUMBER: US/08/516,839

FILING CAMPELIA CAMPERIA CAMPER
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TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 amino acids
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3Y: linear
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RESULT 12 US-08-516-859A-75

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Sequence 72, Application US/08459568
Fatent No. 5911304
Fatent No. 1911304
Fatent No. 1911304
Fatent No. 1911304
Fatent No. 191104
Fatent Proteins
Fatent No. 191104
Fatent No
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FILLICATION NUMBER: US/08/459,568
FILLION DATE: US-7UN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILLION NUMBER: US 08/399,411
FILLION DATE: 06-7AR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathyrn A.
REGISTRATION NUMBER: 31,915
REFERENCE/DOCKET NUMBER: P-1J 1264
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUNESSEE: Campbell and Flores
SIREET: 4370 ta Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October 20, 2003, 13:50:07
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CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                       60.08
60.08
7.00.08
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      (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 535-900 ELEPENA: (619) 535-6349 INFORMATION FOR SEQ ID NO: 7 SEQUENCE CHARACTERISTICS:
TELEPHONE: (619) 535-900
TELEFAX: (6.2) 536-8949
INFCRAMION FOR BOD IL MO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 8 antico acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4, Conservative
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                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                          inear
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| ECLLE 5
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                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                  US-09-528-706-75
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GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION:
APPLICANT:
APPLICANT:
AND SESSED:
CAMPAGE CAUCHOES:
ADDRESSED:
Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21, DB 4, Length 8; Pred. No. 2.5e+05; 1, Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/292,683
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P-LC 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION MADBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 13,1315
REFERENCE/DOCKET NUMBER: 1776
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SEQUENCE DESCRIPTION: SEQ ID NO: 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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; Sequence 75, Application US/09528706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0%;
Matches 4; Conservative
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T-cell receptor be
T-cell receptor be
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macrophage cytotox
T-cell receptor be
biotin A - Citroba
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cerebellar degener
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chlorophyll a/b-bi
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                                             October 20, 2003, 13:11:30 ; Search time 38 Seconds (without alignments) 22.777 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Natch 100%
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Match Length DB

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Perfect score:
Sequence:
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32 11 28.3 9 2 31 10 26.3 4 2 32 10 26.3 4 2 33 10 26.3 6 2 34 10 26.3 7 2 36 10 26.3 7 2 37 10 26.3 7 2 38 10 26.3 7 2 39 10 26.3 7 2 41 10 26.3 7 2 42 10 26.3 7 2 43 10 26.3 7 2 44 10 26.3 7 2 44 10 26.3 8 2 45 10 26.3 8 2 46 10 26.3 7 2 47 10 26.3 8 2 48 10 26.3 8 2 48 10 26.3 8 8 49 10 26.3 8 8 40 10 26.3 8 8 40 10 26.3 8 8 40 10 26.3 8 8 40 10 26.3 8 8 40 10 26.3 8 40 10 26.	A61386 A463360 A26209 H48126 S78024 S78024 C56733 S29735 PC2373 A32523 A32523 A32523 A32523 A32523	ALIG	score Pred.	nese.	ii, Y.; cization :9614425; NID:912	Scc Pr
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C-Cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
Cispedies: Rattus morvegicus (Norway rat)
Cispedies: Rattus morvegicus (Norway rat)
Cibaces: O-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
Cibacession: PRO542
Rigold, D-P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
Cisxp, Med. 174, 1467-1476, 1991
A.Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg;
A.Reference number: PRO891; MJD:92078857; PMID:1836012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rishiwan, D.; Gampbell, A. Gene 67, 203-211, 1988
Gene 67, 203-211, 1988
Affiller Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacte A;Reference number: 140697; MJID:89066280; PMID:2971595
A;Accession: 140697
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A/Title: Unnctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509, MJID:91277601, PMID:1711558
A/Accession: PT0601
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C;Species: Citrobacter freundii
C;Date: i2-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)
Cippedies in Nus musculus (fouse mouse)
CiDate: 17-Uni-1992 #sequence revision 17-Jul-1992 #text_change 30-May-1997
CiAccession: PT0601; PT0617; PT0694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AjMolecule type: mRNA
AjResidues: 1-9 <GOL>
AjXperiduental source: complete Freund's adjuvant-immunized lymph
AjNore: the authors translated the codon TGC for residue 2 as Ala
CjKeywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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A.Accession: P70694
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32.6%; Score 12; D5 2; L
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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A,Molecule type: DNA
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Best Local Similarity
Matches 3, Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
C;Accession: A60427
R;Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol, 19, 704-709, 1991
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin A;Reference number: A60427; MUID:91372335; PMID:1959970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accesion: A61328
R;Br:cteux-Gregoire, S:; Schyns, R:; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema, J
Biochim. Biophys. Acta 386, 244-255, 1975
A;Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaenop
                                elastase - Pseudomonas aeruginosa
C/Species: Pseudomonas aeruginosa
C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C/Accession: 872446
R/Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
PEBS Lett. 299, 291-293, 1929
A/Fittle: Identification of Cleavage sites involved in proteolytic processing of Pseudom:
A/Fittle: Identification of Cleavage sites involved A/Fittle: Identification of Pseudom: A/Fittle: Identification of Cleavage Sites involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing of Pseudom: A/Fittle: Identification of Cleavage Sites Involved In proteolytic processing Involved Inv
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A;Residues: 1-9 <JCN>
A;Note: the sequence from the text on page 706 is inconsistent with that from page 708
C;Reywords: cytokine
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A;Residues: 1-8 «BRI»
(C.Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;i-8/Domain: activation peptide #status experimental «API»
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A,Accession: A61328
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50.0%; Pred
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Best Local Similarity 75.0
Matches 3, Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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Richber, G.; Machee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.; S.ol. Chem. 263, 1140-1145, 1988
M.Filie: Divergence in primary structure between the molecular forms of acetylcholines A; Accession: A34026; MUID: 88087239; PMID: 3335534
A; Mocession: A34026
A; Mocession: A34026
C; Keywords: alternative splicing; carboxylic ester hydrolase
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calsequestrin, fast skeletal muscle - rabbit (fragment)
calsequestrin, fast skeletal muscle - rabbit (fragment)
c)Species: Oryctolagus cunioulus (Somestic rabbit)
c)Accession. B39040
R:Cala. S. E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Tible: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by case A;Reference number: B39040. MUID:91093183; PMID:1985907
                  Cybate: 17-731-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 Cybate: 17-731-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 Cybatesion: PT0533 #sequences of fetal T cell receptor beta chains have few N regions. A.Pfible: Junctional sequences of fetal T cell receptor beta chains have few N regions. A.Pfible: Junctional sequences of fetal T cell receptor beta chains have few N regions. A.Pfates: translation not shown A.Pfates: translation not shown A.Pfates: translation not shown A.Pfates: translation and shown A.Pfates: 1-6 cPEs A.Estiques: 1-
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100.0%; Pred. No. 2.8e+05;
tive C; Mismatches 0;
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Pred. No. 2.8e+05;
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C. Species: Mus musculus (house mouse)
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75.0%;
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Best Local Similarity 75.00
Best Local 3: Conservative
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Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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(Species: Mus musculus (house mouse)
(Spate: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
(Spacession: B3564)
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B.
Proc. Natl. Acad. Sci. US.A. 87, 3031, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal man A;Reference number: A35649, MJD:90222173; PMID:2326268
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A)Title: Junctional sequences of fetal T cell receptor beta chains have few N
A)Reference number: PTO$09; XJID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Mus musculus (house mouse)
C.Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C.Accession: PT0679; PT0708
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                             A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, straim BALB/c, 154-1H
C;Keywords: T-cell receptor
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A;Accession: PT0708
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A,Molecule type: DNA
A,Residues: 1-5 <FE2.
C,Reywords: 1-5 creeptor
C,Reywords: T-cell receptor
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66.7%;
A;Status: translation not shown
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Best Local Similarity 66...
Free 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-6 < CHE>
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us-09-489-760a-1.closed.rpr

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Theograph receptor beta chain V-D-J region (111-1AG) - mouse (fragment)

C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Sacession: Pr0628

R.Feeney, A.J.
Exp. Med. 174, 115-124, 1991

A.A.Reference number: Pr0639, MuID:91277601; PMID:1711558
A.A.Reference number: Pr0639, MuID:91277601; PMID:1711558
A.Scatus: translation not shown
A.Scatus: translation not shown
A.Scatus: A.Scatus: A.S.
A.Sperimental scurce: newborn thymus, strain BALB/C
C.Skeywords: T-cell receptor
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Best Local Similarity 100.
Matches 2; Conservative
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PT0122
T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)
C:Secies: Mus musculus (house mouse)
C:Secies: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0722
B:Feeney, A.J.
C. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MJID:91277601; PMID:1711558
A;Secession: PT0722
A;Status: translation not shown

Ouery Match
31.6%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Xatches 2; Conservative 0; Mismatches 0; Indels A Molecule type: DNA A, Residues: 1-7 eFEE A) Experimental source: newborn thymus, strain BALB/c C, Keywords: T-cell receptor

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Search completed: October 20, 2003, 13:16:33 Job time: 40 secs

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PIR; 140697; 140697.
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COPACTOR: Pythdoxal phosphate.
PATHWAY: Biotin biosynthesis.
SUBUNIT: Homodimer.
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01-JAN-1990 (Rel. 13, Last seq
16-OCT-2001 (Rel. 40, Last ann
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                                                     October 20, 2003, 13:03:44; Search time 24 Seconds (without alignments) 17.635 Million cell updates/sec
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Compugen Ltd.
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Copyright (c) 1993 - 2003
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PPH2_YYCES
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ALL2_CARMA
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UF03_MOUSE
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GFRP_MOUSE
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this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way conflicted and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINES $906280.

Shiuan D., Campbell A.;

Transcriptional regulation and gene arrangement of Escherichia of Circopacter freuddiand Salmonella typhimurium bictin operons.";

Gene 67:203-211(1985).

-1. CATALYTIC ACTIVITY: S-adenosyi-L-methionine + 8-amino-7-cyononanoate = S-adenosyi-L-methylbio-2-oxobutanoate + 7.8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2201 (Rel. 40, Last amnotation update)
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
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larity 100.0%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 0; Indels
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PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
Blotin blosynthesis; Transferase; Aminotransferase;
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Pseudomonas putida
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                                                                         01-NOV-1995 (Rel. 32, Created)
C1-NOV-1995 (Rel. 32, Last sequence update)
C1-NOV-1995 (Rel. 32, Last sequence update)
C1-NOV-1995 (Rel. 33, Last annotation update)
Noosulfakinin-1 (NEB-SK-1).
Sarcophaga bullata (Grey fiesh fly) (Nechellieria bullata).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptexa, Endopterygota, Diptera, Brachycera, Muscomorpha, Oestroidea,
Sarcophagidae, Sarcophaga.
                                                                                                                                                                                                                                                     MEDLINE=93083:01; PubMed=1360367; Ponagy A., Schoofs L., Proost P., van Damme C., de Loof A.; Fonagy A., Schoofs L., Proost P., van Damme C., de Loof A.; Fonagy A., Schoofs L., Proost D., van Damme C., de Loof A.; Comp. Hoofelleria bullata.", Comp. Biochem. Physiol. 103C:135-142(1992).
-:- FUNCTION: MYOTROPIC PEPTIDE.
-:- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
InterPro., IPRO01651; GASTRIN.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
Tyler M.J., Wallace J.C.;
The structure of new peptides from the Australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skin secretion:
whathits P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Crăniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rubelia.";
Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.6%; Score 12; DB 1; Length 9;
100.0%; Pred. No. 1.3e+05;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Neuropeptide; Amidation; Sulfation.

MOD_RES 4 4 SULFATION (POTENTIAL).

MOD_RES 9 9 AMIDATION (FOTENTIAL).

SEQUENCE 9 AA; 1187 MW; 8B0A0691E86BSBAAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RE42 LITRU STANDARD; PRT; 9 AA. P82075; P82093; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) Rubeliidin 4.2/4.3. Litoria rubella (Besert tree frog).
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SUBCELLULAR LCCATION: Secreted.
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Best Local Similarity 100.
Matches 2; Conservative
                                              STANDARD;
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-!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
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DIDINGE=25203287; Pubxed=7895732;

Corbett 5.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.C.;

"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THIS UNKNOWN
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10-FEB.1995 (Rel. 31, Last sequence update)
10-FEB.2010 (Rel. 4C, Last annocation update)
Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
Exiaryoca, Netazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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-:- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-:- PTY: Rubellidin 4.2 seems to differ from Rubellidin 4.3 termina, amidation.
-:- MASS SPECTROMETRY: MW-883; METHOD=FAB.
Amphibian defense peptide; Amidation.
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                               31.6%; Score 12; DB 1; Length 9; 66.7%; Pred: No. 1.3e+05; tive ; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electrophoresis 15:1459-1465(1994).
-!- MISCELLANEOUS: CN THE 2D-GEL THE DETERMINED PI OF
PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 9 AA; 1104 MW; 887451BB5301B2CA CRC64;
                                                                                                                                                                                                                                                                          SEQUENCE 9 AA; 884 WW; 202077205AA72728 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JN-1994 (Rel. 29, Created)
01-JN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
TrpBA operon transcriptional activator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e FA
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MEDLINE=89335826; PubMed=2503057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chery Match
Best Local Similarity Tours
There 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                        0.00 June 31.67
Sest Local Similarity 66.77
Matches 2, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eberly L., Crawford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND SELECT OF SE
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Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN 1S: 6.0, ITS MM 1S: 32 kDa.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FBS-2003 (Rel. 15, Last sequence update)
Transaldolase I (EC 2.2.1.2) (Fragment)
Pichia jadinii (Yeast) (Candida utilis).
Bukaryota; Pungi, Ascomyootas Saccharomyoctina; Saccharomycetes; saccharomycetases; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95009907; PubMed=7523108; Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; "Separation and sequencing of familiar and novel murine proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=77110646; PubMed=556924;
Sun S.C., Joris L., Tsclas O.;
"Purification of crystallization of transaldolase isozyme I and
evidence for different genetic origin of isozymes I and III in
Candida utilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1994 (Rel. 30, Created; 01-0CT-1994 (Rel. 30, Last sequence update) 01-2FB-1995 (Rel. 31, Last amotation update) Juknown protein from 2D-page of fibroblasts (F13) (Fragment). Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11; DB 1; Length 9;
Pred. No. 1.38+05;
1; Mismatches 1; Indels
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                                                                                                                                                                            9 A.
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InterPro; IPR001885; Transaldolase.
PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.9%;
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Best Local Similarity 50.3
Matches 2; Conservative
                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4903;
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ID _UF02_MOUSE
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                                                                                                                                                                                                            This SKISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombyco:dea;
NCBL_TaxID=7091;
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J. Biol. Chem. 275:9892-9892(2000).
-!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCTR (INDOLEGIYOEROL PROSPHATE), TRPI BINDS UPSTREAM OF TREAB OPERON, CVERLAPPING ITS OWN PROMOTER REGION.
SIMILARITY: BELONGS TO THE LYSR PAMILY OF TRANSCRIPTIONAL REGULATORS.
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INDEPPO: IPR006847; HTH LUSR.
PROSITE; PS00044; HTH LUSR_FAXILY; PARTIAL.
TYPODAME Diosynthesis; Transcription regulation; Activator; DNA binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a prothoracicostatic peptide in the larval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C145 X N140, TISSUE-Brain,
MEDLINE=20002634; PubMed=16531308,
Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11, DB 1, Length 6;
Pred, No. 1.3e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.9%; Score 11; DB 1; Lengih 9; 60.0%; Pred. No. 1.3e+65; tive 6; Mismatches 2; Indels
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SEÇÜENCE 6 AA, 683 MW, 77672AA:BDD6F000 CRC64;
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16-OCT-2011 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION.
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J. Biol. Chem. 274:31169-31173(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.9%;
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Matches 3; Conserv
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Best Local Similarity
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P82003:
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OVIDUCT.
-!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBOESCHAGEAL GANGLION.
PIR; A60655; AX.OLM.
Amidation; Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91:47969; PubMed=8313870;
Hughes G.J., Frutiger S., Paquet N., Pasquall C., Sanchez J.-C.,
Hughes G.J., Prutiger S., Paquet N., Posquall C., Sanchez J.-C.,
"Husso J.-D., Balroch A., Appel R.D., Hochstrasser D.F.;
"Husso Ilver protein map: update 1993.";
Electrophoresis 14:1216-1222(1993)
-!- XISCELAREOS: ON THE 2D-682 THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.5, ITS MW IS: 12 KDa.
                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Unknown protein from (D-page of liver tissue (Spot 94) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrbini, Hominidae, Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleccyemata, Brachyura,
Eubrachyura, Portuncidea, Portunidae, Carcinus.
NCB. TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.3%; Score 10; DB 1; Length 9;
larity 100.0%; Pred. No. 1.3e+05;
Conservativo 0; Mismatches 0; Indels
                                                                                                                                           Cuery Mauch
Best Local Similarity 106.0%; Pred. No. 1.38+05;
Mauches 2; Conservative 3; Mismatches 0; Indels
                                                                                          AMIDATION.
387D7DD447ZAB6C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA; 990 MW; FICCTBI72AB6DDCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carcinus maenas (Common shore crab) (Green crab)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                              9 AA; 1060 WW;
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es 2; Conserv
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P61805;
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P31934;
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ALL2_CARMA
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FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
       Caps
                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).
Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Amanoilophyta; eudicotyledons; core eudicots;
Asteridae; Lamids; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. Moneymaker; TISSUE=Seed;
MEDLINE=22361242; PubMed=12473124;
MEDLINE=22361242; PubMed=12473124;
Bozzo G.G., Raghorthama K.G., Flaxkon W.C.;
Bozzo G.G., Raghorthama K.G., Flaxkon W.C.;
Burzification and characterization of two secreted purple acid phosphatase isozymes from phosphate-starved tomato (Lycopersicon beschlentum) cell cultures."

Eur. J. Biochem. 269:6238-6286(2002).

-! - CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = amalcon + phosphate.

-! - SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92179466; PubMed=1796179; Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; "Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP), a novel biologically active neuropeptide from Locusta migratoria.";
                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
01-GUSTA993 (Rel. 27, Last annotation update)
Locustamyouthibiting peptide (LOM-MIP).
Locustam migratoria (Migratory locust).
Eukaryora; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meopteroidea; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Next Acrididae; Oedipodinae; Locusta.
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Pred. No. 1.3e+05;
       1; Indels
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         Xismatches
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         1; Conservative
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1 XEDEI 5
                                             2 LXDDL 6
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-!- FUR
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MEDLINE=92196111; PubMed=1549595;
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UF03 MOUSE
ID _UF03_MOUSE
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
Calliphera vomitoria (3lue blowfly).
Calliphora vomitoria (3lue blowfly).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Calliphoridae, Calliphora.
Calliphoridae, Calliphora.
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TISSUB-Kidney;
MEDIINE-94286447; PubMed-7912428;
Nabline-94286447; PubMed-7912428;
Nadrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"PMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      FARI HELTI STANDARD; PRT; 7 AA.
P41871;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last amnotation update)
10-NOV-1995 (Rel. 32, Last amnotation update)
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--- FUNCTION: APPEARS TO BE INVOLVED IN CSMOREGULATION BY AFFECTING THE KUNBLY, NAVATLE AND SKIN.
--- TISSUE SPECIFICIATY KENDRY, SKIN, MANILE AND THE HEMOLYMPH
--- SIMILARITY: BELONGS TO THE PARP (PMPFAMIDE RELATED FEPTIDE)
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               "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODIVATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD RES
SEQÜENCE 7 AA; 770 NW; 672879CDCB5DDB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9; DB 1; Length 7; Pred. No. 1.3e+05; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                           DB 1; Length 7; . 1.3e+05;
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7 AA; 851 MW; 69040729076AA810 CRC64;
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                                                                                                                                                                                                      23.7%; Score 9; DB 1
103.0%; Pred. No. 1.3
tive 0; Mismatches
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50.0%;
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                                                                                                                                                                                                                               Best Local Similarity 103.
Matches 2; Conservative
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les 2; Conservative
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Thorpe A.;
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FARI_HELTI
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Matches
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MEDLINE=95009907; FubMed=7523.08;
MEDLINE=95009907; FubMed=7523.08;
Memtack B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANBOUG; ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN NOW TERR.
NOW TERR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Crchard I., Rehfeld C.F., Thorpe A., "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 reuropeptides (designated calliPMRFamides) from the blowfly Calliphora vomitoria "., Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
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01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last amontation update)
Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indeis
                                                                                                                                                                                                                                                                                                                                                                                      Score 9; DB 1; Length 7; Pred. No. 1.3e+05; 2; Mismatches 1; Indele
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                                                                                                                                                                                                                                                                                                                           SEQUENCE 7 AA; 926 MW; 69D40699C44AB700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA.
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                                                                                                                                                                                                                                                                                                   AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                         23.7%;
                                                                                                                                                                                                                                  PIR; B44787, B44767.
Neuropeptide; Amidation.
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 25.0 Matches 1: Conservative
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01-OCT-2002 (TrEMBLrel, 22, Created)
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Q81pt5 zea mays (m
Q9xyn0 bacteriopha
Q9fsz2 cioce ariet
O9qza8 mus musculu
Q85710 rous sarcom
Q8ttd7 human immun
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P72279 rhodococus
Q51594 escherichia
Q91634 aspergilus
Q86550 bacteriopha
Q81681 bacteriopha
Q91644 homo sapien
Q91446 macaca neme
Q8aum7 carassius a
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                                                                                                                                                                                                                                                                                          October 20, 2003, 13:10:35; Search time 93 Seconds (without alignments) 24:973 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archeai.*

2: sp_bacteria:*

3: sp_fungi:*

5: sp_invanc.*

6: sp_invanc.*

7: sp_manmal:*

8: pp_bage:*

9: sp_phage:*

8: pp_bage:*

8: pp_vanc.*

8
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QSLPTS

QSLPTS

QSCAR

QSCAR
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
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Match Length DB
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Perfect score:
Sequence:
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ALIGNMENTS

RESULT	7.T :			
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GI.	P82568	PRELIMINARY;	PRT;	9 AA.
AC	P82568;			
EG.	01-CCT-2000		Created)	
EC.	01-OCT-2000	(TrEMBLrel. 15,	Last	sequence update)
5	CI-OCT-20C3	(TrEMBLrel. 15,	Last annot	annotation update)
33	Unknown prot		(Fra	
SS	Streptococcus pyogenes.	is pyogenes.		
ပ္ပ	Bacteria; Fi	Bacteria; Firmicutes; Lactobacillales;	bacillales;	Streptococcaceae;
DO O	Streptococcus.	18.		•
X	NCBI TaxID=1314;	13:4;		
N.E	- [1]			
Ω,	SEQUENCE, AND MASS	OF MASS SPECTROMETRY	STRY.	
<u>ي</u> ي	STRAIN=JRS4;			
R.	Hogan D.A., Du P.,		T.I., whi	Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
KA.	VarBogelen R.A.;			
RT	"Two-dimensional	ional gel electrophoresis	ophoresis m	map of Streptococcus pyogenes
FT	proteins.";			
R.L	Submitted (A	(AY-2000) to the	SWISS-PROT	Submitted (MAY-2000) to the SWISS-PROT data bank.
Ö	-!- MASS SPE	SCTROMETRY: XW=22	2592.04; ME	THOD=ELECTROSPRAY.
[- [1,	NCN TER	г		
į,	NON TER	6		
SC	SEQUENCE	9 AA; 1069 NW;	2A771042CB	2A771042CB1AB2D7 CRC64;
26	Query Match	42.14	Score 16;	DB 2; Length 9;
Σ	Matches 2,	vat	c	
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RESULT	JLT 2			
91	OBLPTS	PRELIMINARY;	PRT;	9 A.A.
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PRT;
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Best Local Similarity 75.0%;
Matches 3; Conservative (
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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01-NOV-1996 (TrEMBLrel.
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     NCEL_TaxiD=3827;
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285710;
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01-MAR-2001 (TrEMBLrel. 16, Last andotation update)
01-MAR-2001 (TrEMBLrel. 16, Last andotation update)
01-MAR-2001 (TrEMBLrel. 16, Last andotation update)
Clost arietinum (Chickpea) (Garbanzo).
Cicer arietinum (Chickpea) (Garbanzo).
Eukaryota, Viridiplantea; Streptophyta, Embryophyta; Tracheophyta; Agnoliophyta; eudicottyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae, Cicer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                  STRAIN=cv. C123; Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S., Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S., Morgante M., Rafalski J.A.; Morgante M., Rafalski J.A.; Experience and linkage disequilibrium in elic maize inbred lines."; Eructure and linkage disequilibrium in elic maize inbred lines."; EMBL/GenBank/DDBJ databases.

EMBL, AY094310; AAX21836.1; --
                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.5%; Score 15; DB 9; Length 9; 40.0%; Pred. No. 8.3e+05; Eive 3; Mismatches 0; Indels
01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Beta-expansin-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TYEMBLYel. 12, Created;
01-NOV-1999 (TYEMBLYel. 12, Last sequence update)
01-DEC-2001 (TYEMBLYel. 19, Last annotation update;
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SEÇÜENCE 9 AA; 1058 MW; 880E376AA720544A CRC64;
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Viruses, dsRNA viruses, Cystoviridae, Cystovirus.
NCBI_TaxID=90889;
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Matches 2; Conservative
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C9FSZ2
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Gorski K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.,

"Derdritic cell regulation of DCL1 mRNA expression.";

"Derdritic (CCT-.199) to the EMBL/GenBank/DD3J databases.

EMBL, AF-09-526; AR-09-943.1;

"MGD, MGI:2136650; Dcl1.
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Lerner T.L., Hanatusa H.;
Lorner T.L., Hanatusa H.;
Larner T.L., Hanatusa H.;
Larner T.L., Hanatusa H.;
Larner of the Bryan high-titer strain of Rous sarcoma virus:
Extent of env deletion and possible genealogical relationship with
other viral strains.";
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCB1_TaxID=10090;
SEQUENCE FROM N.A.
STRAINHEW. Castellana, TISSUE-Etiplated epicotyl;
STRAINHEW. Castellana, TISSUE-Etiplated epicotyl;
Subminer B., Jimenez T., Labrador E.,
"CDA clones expressed in etiplated Cicer arietinum epicotyls.";
Submitted (SEP-2000) to the EMBL/GenBank/PDBJ databases.
EMBL, AC29069; CAC10216.1;
EMPL, AC29069; CAC10216.1;
EMPCHAICAL Protein.

SEQUENCE 9 AA, 990 NW, 9441BDDBA7272EBE CRC64;
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                                                                                                                                                                                                                                                                                                                                     Score 14, DB 10; Length 9, Pred. No. 8.3e+C5; Mismatches C; Indels
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Pred. No. 8.3e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rous sarcoma virus.
Viruses; Retroid viruses; Retroviridae; Aipharetrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-YAY-2000 (TrEMBLrel. 13, Created)
01-YAY-2000 (TrEMBLrel. 13, Last sequence update)
10-DEC-2001 (TrEMBLrel. 13, Last annotation update)
0-type lectin DC11 (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 03, Last annotation update)
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9 AA; 994 XW; 342161AB172EBAB7 CRC64;
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MEDLINE-99255622, PubMed-7737502,
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Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the IncFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=33008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 13; DB 2; Length 8; 33.3%; Pred, No. 8.3e+55; tive 3; Mismatches 1; Indels
                                                                                                           Length 7;
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"Incompatibility repressor in a repA-like replicon of plasmid Colv2-K94.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEC-2001 (TrEMBLrel. 19, Last annotation update)
Biphenyl dioxygenase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0:-NOV-1996 (TrEMB_rel. 01, Created)
0:-NOV-1996 (TrEMB_rel. 01, Last sequence update)
0:-DBC-2011 (TrEMB_rel. 19, Last annotation update)
Cop8 protein (Fragment).
                                           7 AA; 899 MW; 672721F6CB572030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 8 AA; 989 XW; EBD2CB1AB6D73406 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
8 AA; 998 MW; 0F37205AA73416D7 CRC64;
                                                                                                    34.2%; Score 13; DB 8; I 42.9%; Pred. No. 8.3e+05; tive 1; Mismatches 3;
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DB
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EMBL; M13472; AAA23194.1; -.
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MEDLINE=86223772; PubMed=2423502;
                                                                                                                                      Local Similarity 42.9
les 3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 33.3
es 2; Conservative
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                                                                                                                                                                                                                                                                               Plasmid ColV2-K94.
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NON TER
SEÇÜENCE 8 ,
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NON TER
SEQUENCE
          NON TER
SEQUENCE
                                                                                                        Query Match
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P72279;
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Q51594;
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Matches
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Q51594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eure.eostomi;
Actinopterygii, Neopterygii; Teleostei; Eureleostei; Roceleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
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                                                                                                                                      Length 9;
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                                                                                                                               36.8%; Score 14; DB 15; Length 9; 50.0%; Pred. No. 8.3e+05; tive 1; Mismatches 2; Indels
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9 AA; 1102 MW; 186BD40B17272440 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                        NON TER 1 1
SEQÜENCE 9 AA; 949 MW; 94AA1443DED731AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA.
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Mol. Phylogenet. Evol. 13:289-301(1999)
EMBL; AF002591; AAD01074.1;
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EMBL; K03365; AAA42557.1; -.
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01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.-MAR.2002 (TrEMBLrel. 20, 01-MAR.2002 (TrEMBLrel. 20, 01-OCT.2002 (TrEMBLrel. 22,
                                                                                              Ouery Match
Best Local Similarity 50.v
نامد :
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Gnatholebias zonatus.
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Best Local Similarity
Matches 3; Conserv
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3 NLLE 6
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VPU.
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08UTD7;
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Local Similarity 50.0
es 2, Conservative
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Matches 2; Conservative
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                                     PRELIMINARY;
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SEQUENCE FROM N.A.
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TISSUE=Brain;
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                                       Cerek1
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Matches
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09BQT4
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"Genomic region with genes 30.6-30.3 of T4-related bacteriophages.";
"Genomic region with genes 30.6-30.3 of T4-related bacteriophages.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Now TER 8
SEQUENCE 8 AA, 918 MW, F3B1A72041B76336 CRC64;
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              Gaps
                                                                                                                                                                                                    Aspergilius flavus.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergilius.
VCBI_TaxID=5059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piesiniene L., Kolesinskiene G., Truncaite L., Zajanckauskaite A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
NCBI_TaxID=12353;
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                                                                                                                                                                                                                                                                                                        Geiser D.M., Dorner J.W., Horn B.W., Taylor J.W.;
"The phylogenetics of mycocoxin and sclerotium production in Aspergillus flavus and Aspergillus oryzae.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF261861; AAG16135.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%; Score 13; DB 3; Length 8; 50.0%; Pred. No. 8.3e+05; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.2%; Score 13; DB 9; Length 8; 50.0%; Pred. No. 8.3e+05; ative 1; Mismatches 1; Indels
             Indels
                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TrpC polyprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Pred. No. 8.3e+05;
2; Mismatches 0;
                                                                                                                              8 A.A.
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7.
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01-JUN-2002 (TrEMBLrel. 21, Last sequ
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Intron, minor histocompatibility antigen HA-1, typing allele, H allele, R allele, polymorphic nucleotide, HA-1 typing, bone marrow transplant, severe aplastic anaemia, leukaemia,
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                                                                                                                                                                                antigen HA-1 R-allele. The specification describes methods for typing alleles (preferably the H and R alleles) of the minor histocompatibility antigen HA-1 in a sample, which comprise detecting polymorphic nucleotides in the cDNA or genomic nucleic acids of the alleles. The methods can be used for HA-1 typing for bone marrow transplants, severe aplastic anaemia, leukaemia and immune deficiency diseases, as well as ablactection of genetic aberrances. The probes and primers of the invention can be used to screen for the HA-1 alleles. The HA-1 peptides can be used anti-idiotypic B cells and/or T cells and antibodies.
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Typing minor histocompatibility antigen HA-1 - by amplifying identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection of genetic aberrances
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Pred. No. 9.3e+05;
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                                                                                                             Claim 13; Fig 5; 59pp; English.
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detection of genetic aberrances. The probes and primers of the can be used to screen for the HA-1 alleles. The HA-1 peptides used anti-idictypic B cells and/or T cells and antibodies.
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                                                                                                                                                                                                    94.7%; Score 36; DB 20; Length 9; larity 88.9%; Pred. No. 9.3e+05; Conservative 0; Mismatches 1; Indels
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Mon Oct 20 14:02:10 2003

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The present sequence represents a new peptide (PI) constituting a T-cell peptiope obtainable from the minor histocompatibility antigen 49-1. The peptide is immunogenic and can be used as part of a vaccine. Pl is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the trearment of severe aplastic annexna, leukaemia, and immune deficiency
                  Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anaemia; immune deficiency disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 20; Length 9; Pred. No. 9.3e+05; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                  Hunt DF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 32; 47pp; English
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                                                                                                                                                                                                                               97EP-0202303.
                                                                                                                                                                                                                                                                                                  Goulmy EAJM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                Engelhard VH,
                                                                                                                          WC9905174-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a new peptide (F1) constituting a T-cell septide obtainable from the minor histocompatibility antigen HN-1. The peptide is immunogenic and can be used as part of a vaccine. Pl is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency
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immune diseases and prevent rejection and host versus graft disease
in bone marrow and organ transplantation
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                                                                                                                                                                                           Minor histocompatibility antigen HA-1 T-cell epitope #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.7%; Score 36; DB 20; 100.0%; Pred. No. 9.3e+05; Live 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hunt DF;
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                        AAW99195 standard; peptide; 9 AA
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Best Local Similarity
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1 VLXDDLLEA
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                                                                                                                                                                                                                                                                                                                                                      Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Engelhard VH,
                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                    RESULT 4
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The 103P3E8 polynucleotide, its related

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Length 9; 0; Indels

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Sequences AAU71093-AAU71796 represent the 103P3E8-related protein and peptide fragments of the protein. 103P3E8 exhibits tissue specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, bladder, kidney, colon, lung, breast, rectum and stomach. The 103P3E8 polynuciectide, its related protein and peptide fragments and specific. PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynuciectide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P2E8-related protein, and a ribozyme capable of cleaving a polynuclectide having the 103P3E8 coding sequence, are both useful in the preparation of a composition for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18389388; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
lung, breast, rectum and stomach. The 103P3E8 polytuoleotide, its relate protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polymulospecifically binds to an 103P3E8 related protein, and a ribozyme apable of Cleanwing a longuable chain monoclonal antibody, that immunospecifically binds to an 103P3E8-related protein, and a ribozyme are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P3E8. The sequences can be used the diagnostic methods to monitor the level of 103P3E8 gene products in serum, blood, usine and tissue and to thereby detect the presence of cancerous cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumcur, cancer, cytostatic, gene therapy, antibody therapy, ribozyme,
şingle chain monoclonal antibody, serum, blocd, urine, tissue, human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monitoring 103P3E8 gene products in sample from patient (suspected obvying cancer, useful for diagnosing, managing or treating cancers, e.g. prostate cancer, comprises determining presence of aberrant 103P3E8 gene products.
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Pred. No. 9.3e+05;
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103P3EB; prostate; bladder; kidney; colon; lung; breast; rectum; stomach; tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme; single chain monoclonal antibody; serum; blood; urine; tissue; human;
                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a new peptide (PI) constituting a T-cell epitope obtainable from the minor histocompatibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. PI is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                       A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 1;
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                         Hunt DF
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                                                                                                                                                                                                                                                                                                        Disclosure; Page 15; 47pp; English
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                         Goulmy EACM,
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103P3E8 gene products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 9q13-q21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 A.A.;
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                      Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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Afar DEH;

Mitchell SC,

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AAU09449 standard; peptide; 9 AA
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patient with a cancer that expresses 103P3E8. The sequences can be used in diagnostic methods to monitor the level of 103P3E8 gene products in serum, blood, utine and tissue and to thereby detect the presence of cancerous cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-A2 resistant tumor antigen peptides derived from SART-1, useful as preventives or diagnostics for tumors e.g. flat epithelloma like lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA-A2 restricted tumour antigen; SART-1; human leukocyte antigen; human; diagnosis; tumour; cytotoxic T cell; flat epithelioma; lung cancer; oesophagus cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY80148 to AAY80181 represent specifically claimed HLA-A2 restrictumour antigen peptides derived from SART-1. The peptides have cytostatic activity. The peptides are useful as a preventive or diagnostic for tumours e.g. flat epithelioma like lung cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-A2 restricted tumour antigen peptide derived from SART-1 #15.
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                                                                                                                                                60.5%; Score 23; DB 23; Length 9; 100.0%; Pred. No. 9.36+05; Eive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 41; 55pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                              AAY80162 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUMU ) SUMITOMO PHARM CO LID. (ITOH/) ITCH K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0212940.
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Best Local Similarity 71.4
S; Conservative
                                                                                                                                                         Cuery Match
Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                    9 AA;
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                                                                                                                                                                                                                                                                                                                                                      RESULT 9
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RESULT 10 AAU09449

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                                                                                                                                                             ATP binding cassette, secretary locus open reading frame; endopeptidase; secretary locus ORF; procease, metalloprotease; CLP procease AfPase; CLP procease subunit; transplay/colase/transpeptidase; CLPC protease; thioredoxin; Chlamydia infection; antibacterial; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ot
                                                                                                          Chlamydophila pneumoniae T-cell epitope #4 useful as Chlamydia antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of Chlamydophila pheumoniae strain CML029 genes and their encoded proteins. The genes the invention encode an ATP binding cassette gene, a secretary locus open reading frame (ORF), an endopeptidase, a protease, a metalloprocease, CLP protease ATPase, a CLP protease subunit, a transglycolase/transpeptidase, a CLPC protease, or thioredoxin. The genes of the invention can be used in a vector as a vaccine for the prevention and treatment of Clamydia infections. AAU09440-AAU09473 represent B. or T-cell epitopes from the C. pneumoniae proteins (AAU09430-AAU09439) of the invention. These epitopes can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine useful for immunising mammals against chlamydia infections, comprises vectors having sequences of ATP binding cassette gene, secretary locus open reading frame gene of chlamydia
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                                                                                                                                                                                                                                                                                                              Chlamydophila pneumoniae CWLC29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2000, 2000US-202672P.
30-MAY-2000, 2000US-217952P.
16-JUN-2000, 2000US-211797P.
16-JUN-2000, 2000US-211797P.
16-JUN-2000, 2000US-211798P.
16-JUN-2000, 2000US-212044P.
26-SEP-2000, 2000US-23535P.
26-SEP-2000, 2000US-235361P.
26-SEP-2000, 2000US-235398P.
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                                                        (first entry)
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                                                     26-MAR-2002
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AAU09449;
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ABP75298
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The present invention describes a method (M1) for the isolation of a subset of peptides from a protein peptide mixture (P1). M1 involves:

(a) separating the protein peptide mixture [P1). M1 involves:

(c) chromatography: (b) chemically, or enzymatically, or chemically and chromatography; (c) chemically, altering at least one amino acid of at least one of the peptides; and (c) isolating the altered generating a subset of altered control of the peptides; and (c) isolating the altered (flagged) peptides out of each fraction via chromatography, where the chromatography of steps (a) and (c) isolating the altered (flagged) peptides out of each fraction via chromatography, where the chromatography of steps (a) and (c) isolation and determination of peptides from protein peptide of the isolation and determination of peptides from protein peptide (c) is performed with the same type of chromatography, M1 can be used for the isolation and determination of proteins indicative of a disease of protein marker or a specific set of proteins indicative of a disease state. M1 can be used for identifying target proteins present in the cannot marker or a specific set of proteins indicative of proteins of proteins of intracellular changes in cells with physiciogical changes such as metabolic shift, in the identification of bromaters in cannoers and in the identification of congest on the need for multidimensional chromatography and without the use of affinity tags. Assemblification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteome analysis, isolation, determination, diagnostic assay, detection, protein marker, identification, metastatic, invasive cancer, differential expression, signalling pathway, chromatography.
                                                                                                                                                                                                                                                             Method for isolation of peptides from complex mixture of peptides involves specific chemical and/or enzymatic alteration of at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.9%; Score 22; DB 24; Length 9; 71.4%; Pred. No. 9.3e+05; Live 0; Mismatches 2; Indels
                                                                                                                  (VLAA-) VLAAMS INTERUNIVERSITAIR INST STOTECHNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteome analysis related peptide #466.
                                                                                                                                                                                                                                                                                                                                                    Example 22; Page 150; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP75181 standard; Peptide; 9 AA.
                   22-MAR-2001, 2001US-278171P.
12-SEP-2001, 2001US-318749P.
20-SEP-2001, 2001US-323999P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuery Match
Best Local Similarity 71.4%,
Best S; Conservative
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                                                                                                                                                                                                                                                           Method for isolation
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                                                                                                                                                                 Vandekerckhove J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLDJESE
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                                                                                                                                                                                                                                                                                                            type of peptide
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A3P75181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method (MI) for identifying secreted intracellular bacterial proteins (BP). MI comprises: (a) selectively visualising BP by pulse labelling in the presence of an inhibitor of eukaryotic protein synthesis followed by 2D electrophoresis and autoradiography; (b) comparing protein profiles (PF) of purified bacteria to PF of total lysate (TL) of infected cells; and (c) identifying protein spots aresent in differential images from gels loaded with TL. The present sequence is one such bacterial peptide epitope which was identified by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteome analysis; isolation; determination; diagnostic assay; detection; protein marker; identification; metastatic; invasive cancer; differential expression; signalling pathway; chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying intracellular bacterial proteins by labeling proteins in the presence of a eukaryotic protein synthesis inhibitor, performing electrophoresis, autoradiography and comparing profiles to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                         Antibacterial; secreted protein; intracellular bacterium.
                                          Chlamydia pneumonia peptide epitope #64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteome analysis related peptide #423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 34; Page 151; 179pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infected-cell lysate profile
                                                                                                                                                                                                                                                                                                                                09-APR-2001; 2001DK-0000581, 09-APR-2001; 2001US-282513P,
                                                                                                                                                                                                                                                                                   09-APR-2002; 2002WO-DK00234
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vandahl BB;
                                                                                                                                                                                                                                                                                                                                                                                                   (SHAW/) SHAW A C.
(VAND/) VANDAHL B B.
                                                                                                                                      Chlamydia pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-058585/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shaw AC,
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Gaps

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RESULT 12 ABP75138

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The present invention describes a method (M1) for the isolation of a subset of peptides from a protein peptide mixture (P1). X1 involves:

(a) separating the protein peptide mixture into fractions of peptides used chromatography; (b) chemically, or enzymatically, or chemically and enzymatically, or chemically and enzymatically, or chemically and enzymatically, or chemically and chromatography; (b) chemically, thereby generating a subset of altered peptides in each fraction, thereby generating a subset of altered peptides and chromatography, where the chromatography of steps (a) and fraction via chromatography, where the chromatography of steps (a) and (c) is performed with the same type of chromatography of steps (a) and c) is performed with the same type of chromatography. MI can be used for the absence or a variation in expression level of at least one protein marker or a specific set of proteins indicative of a disease state. MI can be used for identifying target proteins present in metastatic and invasive cancers, in differential expression of proteins in transgenic mice, identification of proteins that are upregallated or changes in cells with physiciogical changes such as metabolic shift, in the identification of biomarkers in cancers and in the identification of biomarkers in cancers and in the identification of containing pathways. The method is gel-free methodology for qualitative and quantitative proteome analysis without the need for multiply mand without the use of affiliative and proteins proteins and proteins and the proteins and proteins and the proteins and the proteins and 
                                                                                                                                                                                                                                                                                                                                                                                    Method for isolation of peptides from complex mixture of peptides involves specific chemical and/or enzymatic alteration of at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP74714 to ABP75190 represent peptide sequences used in the exemplification of the present invention.
                                                                                                                                                                                               (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 22; Page 151; 193pp; English.
                                                                                                                                                                                                                                                             Gevaert K;
                                                                 22-MAR-2001, 2001US-278171P.
12-SEP-2001, 2001US-318749P.
20-SEP-2001, 2001US-323999P.
22-MAR-2002; 2002WO-EP03368
                                                                                                                                                                                                                                                                                                                         WPI; 2003-067379/06.
                                                                                                                                                                                                                                                          Vandekerckhove J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      type of peptide
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Gaps ., .3e+05; Score 22, DB 24, Length 9, Pred. No. 9.3e+05, Mismatches 2; Indels 57.9%; Scor 71.4%; Pred 0; 1 5, Conservative Query Match Best Local Similarity

2 EXPORTS 8 TIDDLSE ટે

AAB12035 standard; Peptide; 6 Ah AAB12035;

17-JAN-2001 (first entry)

Peptide # 2 used in PR domain peptide analysis.

Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease; cell proliferation; cell differentiation; tissue repair; PR domain; transcription regulator; breast cancer; gene therapy; melanoma; neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease; Alzheimer's disease; paralysis; motor neurone disorder.

Unidentified

US6069231-A.

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phosphostoma (Rb)-interacting zinc finger (RIZ) protein is a nuclear phosphoprotein that acts as a cell differentiation factor. RIZ can modulate cell growth by binding to Rb protein, which is involved in regulating cell proliferation. In addition, RIZ can act to regulate transcription. RIZ functions to maintain cells in the Gl phase of the transcription. RIZ functions to maintain cells in the Gl phase of the cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ protein is a PR domain protein and is present primarily in the cell nucleus. RIZ gene mutations may be implicated in various cancers such as melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may use through for these disorders. Since RIZ protein is implicated in cell cycle arrest, inhibition of RIZ activity may be useful in meurodegenerative disorder therapy e.g. for Parkinson's, Huntingdon's or Alabeimer's disease, paralysis or motor neurone disorders, or cardiac disorders e.g. heart disease, where the ability to induce neural/ cardiac used in the analysis of PR domain peptides of the present invention.
                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                New PR domain peptides comprising amino acid sequences from, for example retinoblastoma-interacting zinc finger, or egi-43 proteins, fregulating gene transcription and controlling cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 21; Length 6;
Pred. No. 9.3e+C5;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Columns 87-88, 91pp, English.
                                                                                                                                                          (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                               94US-0292683.
95US-0399411.
                                                         95US-0516859.
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                                                                                                                                                                                                                                                                                                                        regulating gene
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                                                         18-AUG-1995;
                                                                                               18-AUG-1994;
                                                                                                                    06-MAR-1995;
                30-MAY-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                    Huang S;
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AAU80810 standard; Peptide; 6 AA (first entry) ECLLE 26-MAR-2002 AAU80810; RESULT 15 AAU80810

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Rat Rb-interacting zinc finger (RIZ) ElA related motif #2.

Rat; human; retinoblastoma protein-interacting zinc finger protein; RIZ; RRDI-BP1; human positive regulatory domain I-binding factor 1; EVI-1; human ecotropic viral integration site-1 myeloid transforming gene; Rb; Caenorhabditis elegans; egī-43; retinoblastoma protein; cardiac muscle; cell proliferation; neural cell; paralysis; neuralegenerative disease; Parkinson's disease; Huntington's disease; Alzheimer's disease; motor neuron disorder; mouse; BIA; cel; crl; crl; GTPase; SH3-binding motif.

Rattus sp.

US6323335-B1

1002-VCN-72

us-09-489-760a-1.closed.rag

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The invention relates to a nucleic acid molecule encoding a FR domain peptide present in human and rat retinoblastoma protein-interacting zinc finger protein (RIZ), PRDI-BFI (human postive regulatory domain. I-binding factor I), 2V.-1 (human enciroptive in regulatory domain. myeloid transforming gene product) or Caenorhabditis elegans egl-43 gene product. The DNA of the invention is involved in regulating transcription of a target gene. RIZ acts as a cell-differentiation factor and modulates a function of a cell by binding to retinoblastoma (Rb) protein, which is involved in regulating call proliferation in various human diseases or conditions, e.g. cancer. RIZ regulates the growth of normal addit cardiac muscle cell death. RIZ les expressed in neural call dowing useful for healing after highry of neural tissue and for treating neurodegenerative diseases such as Parkinson's, Huntington's or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease and paralysis, or motor neuron disorders through induced or decreased proliferation of neural celis. The PR domain or RIZ active fragment containing a PR domain is useful as a probe to identify transcription factors or oncogenic proteins in a cell that bind the PR domain. Sequences AAU80803-AAU80854 represent protein and peptide
                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule comprises the code for a conserved domain of retinoblastoma protein-interacting zinc finger protein, positive regulatory domain I-binding factor involved in regulating gene
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3, Column 35, 93pp, English
                                                               18-AUG-1995; 95US-0516859.
17-MAR-2000; 2000US-0528706.
18-AUG-1994; 94US-0292683.
06-MAR-1995; 95US-0399411.
                     01-JUN-2000; 2000US-0586472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecules of the invention.
                                                                                                                                                                                                                                                              WPI; 2002-096600/13
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                                                                                                                                                                               (HUAN/) HUANG S.
                                                                                                                                                                                                                                                                                                                                                                                   transcription
                                                                                                                                                                                                                           Huang S;
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Gaps . O

55.3%; Score 21; DB 23; Length 6; 80.0%; Pred. No. 9.3e+05; 11ve 1; Mismatches 3; Indels

Query Match Sest Local Similarity 80.0 Matches 4; Conservative

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े g Search completed: October 20, 2003, 13:13:36

Job time : 82 secs

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Sequence 349, Appl
Sequence 169, Appl
Sequence 170, Appl
Sequence 171, Appl
Sequence 171, Appl
Sequence 173, Appl
Sequence 173, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
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Sequence 349, App
Sequence 54, Appl
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                                                                                                                                    October 20, 2003, 13:15:55 ; Search time 65 Seconds (without alignments) 22:696 Million cell updates/sec
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| cgn2_6/prodate/2/pubpaa/VSC7_PJBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/PCT Ra* PUB.pep:*
| cgn2_6/prodate/2/pubpaa/SCT NEW PUB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG NEW PUB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG NEW PUB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG NEW PUB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG NEW PUB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG NEW PUB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG PUBCOMB.pep:*
| cgn2_6/prodate/2/pubpaa/JSG PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-834-765-349

2 US-09-834-765-348

2 US-10-166-225A-169

2 US-10-166-225A-170

2 US-10-166-225A-172

2 US-10-166-225A-172

2 US-10-166-225A-173

2 US-10-166-225A-173

2 US-10-166-225A-173

2 US-10-171-708-8

US-09-801-784-21

US-09-801-784-21

US-09-801-784-22

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                                                                                                                                                                                                                                                                                                                                                                                                                 609562 segs, 163917102 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                using sw model
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Gapop 10.0 , Gapext 0.5
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38
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Match Length 33
                                                                                                                                                                                                                                                                                         1 VLXDDLLEA 9
                                                                                                OM protein - protein search,
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                                                                                                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                                                                                                                                         Sequence:
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CC	equence 394 Sequence 2954, Sequence 3914, Sequence 3915, Sequence 3915, Sequence 3916, Sequence 3917,	777, 115, 116, 132, 332, 41, 41, 41, 41, 41, 41,
5-10-044-692-14 5-10-044-539-14 -09-989-789-295 -09-989-789-387 -09-989-789-391 -09-989-789-391 -09-989-789-391	09-989-789-39 -09-990-186-2 -09-990-186-3 -09-990-186-3 -09-990-186-3 -09-990-186-3 -09-990-186-3	7 T T T T T T T T T T T T T T T T T T T
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ALIGNMENTS

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0
                                                                               Sequence 132. Application US/09834765
Patent No. USC0200554881
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Archur B. Raitano
APPLICANT: Archur B. H. Afar
APPLICANT: Archur Archur And DeTECTION OF CANCER
FILE REFERENCE: 129.6USU1
FILE REFERENCE: 129.6USU1
CURRENT APPLICATION NUMBER: 60/197,647
PRIOR APPLICATION NUMBER: 60/197,647
PRIOR APPLICATION NUMBER: 60/197,647
PRIOR FILMO BATE: 2000-64-12
PRIOR FILMO BATE: 2000-64-12
FILMORENT FILMOR BATE: 2000-64-12
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FILMORENT FILMORE ARCHUR BATE: 2000-64-12
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100.0%; Pred. No. 5.4e+05;
vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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US-09-834-765-132
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Best Local Similarity
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RESULT 1
US-C9-834-765-132
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RESULT 2 US-39-834-765-349 ; Sequence 349, Application US/09834765

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APPLICANT: BERRY, Alan
APPLICANT: HUMBELLN, Markus
APPLICANT: LOPEZ-ULIBRRY, Rual
APPLICANT: MAYER, Anne F.
APPLICANT: WELISERV, Alexei A.
TITLE ONE TOWENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REFRENCE: 038435/121966
UNRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NGS: 197
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT BERRY, Alan
APPLICANT BERRY, Alan
APPLICANT BREATZEL, Werner
APPLICANT HUBBELIN, Warkus
APPLICANT HUBBELIN, Warkus
APPLICANT HUBBERN, Rai
APPLICANT WELLSERV, Alexen A.
TITLE OF INVENTION INFROVED ISOPRENDID PRODUCTION
FILE REFERENCE: C184435/121966
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NCS: 197
SCPTWARE: Patentin Version 3.1
SEC ID NO 169
                  APPLICANT: XAYER, Arne F.
APPLICANT: YELISEBY, Alexei A.
TITLE OF INVANTION: IMPROVED ISOPREMOID PRODUCTION
FILE REPERRICE: C30435/121966
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 2022-06-05
NUMBER: Patentin Version: 3.1
SEQ ID NO 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%; Score 20; DB 12;
60.0%; Pred. No. 5.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; CAGANISM: Rhizobium sp. strain NGR234
US-10-166-225A-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     // Sequence 169, Application US/10166225A
// Publication No. US20030148416A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Sequence 170, Application US/10166225A ; Publication No. US20030148416Al ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        ORGANISM: Bradyrhizobium japonicum
LCPEZ-ULIBARRI, Rual
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0.
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Best Local Similarity 60.0
Matches 3, Conservative
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US-10-166-225A-169
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0
                                     GENERAL INFORMATION

APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Daniel E.H. Afar
APPLICANT: AND JETECTION OF CANCER
FILE REFERENCE: 129.6USUJ
CURRENT APPLICATION NUMBER: US/09/834,765
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 770
SEQ ID NO 349
SEQ ID NO 349
SEQ ID NO 349
SEQ ID NO 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.3%; Score 21; DB 12; Length 9; 80.0%; Pred. No. 5.4e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%; Score 23; DB 9; Length 9; 100.0%; Pred. No. 5.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54, Application US/C9833203
| Publication No. US2030166277A1
| GENERAL INFCRMATTON:
| GENERAL INFCRMATTON:
| APPLICANT: Sauderer, Maurice |
| TILE REFERENCE: INSONER: US/O9/833,203 |
| CURRENT APPLICATION NUMBER: US/O9/833,203 |
| PRIOR PELING DATE: 2000-04-12 |
| PRIOR FILLNG DATE: 2000-04-12 |
| NUMBER OF SEC ID NOS: 63 |
| SEQ ID NOS: 63 |
| SEQ ID NOS 64 |
| LENGTH: 9
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US-10-166-225A-168
S-10-166-225A-168
S-26quence 168, Application US/10166225A
Publication No. US20030148416A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
; CTHER INFORMATION: C35 peptides
US-09-833-203-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BERRY, Alan
APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.5
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens US-09-834-765-349
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| DLIEA 5
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) Publication No. US2003016220241
) GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: SIJO, Yen
APPLICANT: BALACUERAMANIAN, SHANKAR
APPLICANT: BALACUERAMANIAN, SHANKAR
APPLICANT: BALACUERAMANIAN, SAFE
APPLICANT: SAPICANTON SAFE
APPLICANT: SAPICANTON SAFE
APPLICANT: SABLO36/01US (8325-2014.01)
CURRENT PELLOS SABLO36/01US (8325-2014.01)
CURRENT FILLNS DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Version 3.2
SEQ ID NOS: 48
SEQ ID NOS: 48
SEQ ID NOS: 48
SEQ ID NOS: 48
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                                                                                                                                                                                                                                       JEMERAL INFORMATION:
JEMERAL INFORMATION:
APPLICANT: BRETZEL, Werner
APPLICANT: HYMBELIN, Warkus
APPLICANT: HYMBELIN, Warkus
APPLICANT: AXYER, Anne F.
APPLICANT: YELISEEV, Alexei A.
ITTLE OF INVENTION: INFROVED ISOPRENCID PRODUCTION
FILE REFERSTCE: C08435/121966
CURRENT APPLICATION NUMBER: US/13/166,225A
CURRENT FILING DATE: 2002-36-05
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 173
LENGTH: S.
                                                                                                                                     RESULT 9
US-10-166-225A-173
Sequence 173, Application US/10166225A
Publication No. US20030148416A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT;
CRSANISM: Haemophilus influenzae
US-10-166-225A-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Fi residue US-10-271-708-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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US-09-801-784-19
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                                                                                                                                     52.6%; Score 20; DB 12; Length 5; 60.0%; Pred. No. 5.40+05; artive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BRERY, Alan
APPLICANT: BRERY, Alan
APPLICANT: HUMBELIN, Werner
APPLICANT: HUMBELIN, Markus
APPLICANT: HUMBELIN, Markus
APPLICANT: NAYER, Anne F.
APPLICANT: NAYER, Anne F.
TITLE OF INVENTION: IMPROVED ISOPRENCID PRODUCTION
FILE REPRENCE: C38435/121966
CURRENT APPLICATION NUMBER: U5/10/166,225A
CURRENT FILING DATE: 2022-06-05
NUMBER OF SEQ ID NOS: 197
SOFTWARR: PATENTIN Version 3:1
SEQ ID NO 172
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BERRY, Alan
APPLICANT: BERRY, Alan
APPLICANT: HUMBELIN, Markus
APPLICANT: HUMBELIN, Markus
APPLICANT: HOWELLN, Markus
APPLICANT: NAYER, Anne F.
APPLICANT: NAYER, Anne F.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REFERENCE: C18435/1966
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 202-06-05
NUMBER OF SEQ ID NOS: 197
SEQ ID NO 171
LENGTH: 5
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| SEQ ID NO 170
| LENGTH: 5
| TYPE: PRT
| ORGANISM: Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                               Sequence 171, Application US/10166225A Publication No. US20030148416A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 172, Application US/10166225A Publication No. US20030148416A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Escherichia coli
US-10-166-225A-172
                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0
Matches 3, Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.6%; Score 20; DB 9; Length 8; 80.0%; Pred. No. 5.4e+05;
                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
CPERATING SYSTEX: PC-DGS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FCOPPY disk
COMPUTER: IBM FC compatible
OPERATING SYSTEX: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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COLI CS4-CFA/I FAMILY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/801,784
FILING DATE: 09-Mar-2001
CLASSIFICATION: «CURNOWIDA ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/801,784
FILING DATE: 09-Mar-2001
CLASSIFICATION: <URKNOWI>
                                                                                                                                                                                                                                  NAME: Hendricks, Glenna M.
REGIETRATION NIMBER: 32.535
REFERENCE/COCKET NUMBER: cas801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-8405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: cas801 TELECCMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCCANISM: E. COLI
STRAIN: CS4-CFA/I
SEQUENCE DESCRIPTICM: SEQ ID NO: 20:
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NAME: Hendricks, Glenna M.
REGISTRATION NUMBER: 32.535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cassels, Frederick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/09801784 Patent No. US20010014668A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           TELBFAX: (702) 425-8406
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks &
STREET: P.O. BOX 2509
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLGGY: unknown
MCLEGULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
GRIGINAL SOURCE:
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Flogg
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amine acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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US-09-801-784-21
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Loomis-Price, Lawrence
TITLE OF INVENTION: PEPTIDES FROM A CONCENSUS PEPTIDE OF
                                                                                       Loomis-Price, Lawrence
TITLE OF INVENTION: PEPTIDES FROM A CONCENSUS PEPTIDE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Irdels
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                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/801,784
FILING DATE: 09-Mar-2001
CLASSIFICATION: «URKNOW»>
                                                                                                                                                   COLI CS4-CFA/I FAMILY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLI CS4-CFA/I FAMILY PROTEINS
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Pred. No. 5.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hendricks, Glenna M.
REGISTRATION UNDARR: 32.535
REFERENCE/DOCKET NUMBER: CASSOI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMTI-SENSE: NO
CRIGINAL SOURCE:
OROANISM: E. coli
STRAIN: CS4-CFA/I
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-601-784-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Hendricks and Assoc.
STREET: P.O. Box 2509
                                                                                                                                                                     NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Hendricks and Assoc.
STREET: P.O. Box 2509
CITY: Fairfax
                                                                APPLICANT: Cassels, Frederick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 425-8405
TELEFAX: (702) 425-8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09801784 Patent No. US20010014668A1 GENERAL INFORMATION:
Sequence 19, Application US/09801784 Patent No. US20010014668A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 8 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
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US-09-801-784-20
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Gaps

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GENERAL ANTONIALIZATION ARTHUR
APPLICANT CHALLITA-EID, PIA M.
APPLICANT CHALLITA-EID, PIA M.
APPLICANT FARIS, MARY
APPLICANT SAFRAN, DOUGLAS
APPLICANT APPLICANT APPR.
APPLICANT APPLICANT APPLICANT BOUGLAS
APPLICANT HUBERT, RAME
APPLICANT HUBERT, RAME
APPLICANT BOUGLAS
APPLICANT APPLICANT AND CATESPONDING PROTEINS ENTITLED
TITLE OF INVENTION NOTECTION OF CANCER
TITLE OF INVENTION DETECTION OF CANCER
TITLE OF INVENTION BAPPLA AND
TITLE OF INVENTION WABER 60/09/932,165
CURRENT APPLICATION NUMBER 60/09/932,165
CURRENT FILING DATE: 2001-08-17
FRING APPLICATION NUMBER 60/226,329
FRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SCOFFWARE PARCENTIN VEY. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1239
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                                          52.6%; Score 20; DB 9; Length 8; 80.0%; Pred. No. 5.4e+05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 20, 2003, 13:25:31
                                                                                                                                                                                                                                                                   Sequence 1239, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Seguence
                     Query Match
Best Local Similarity 80.07
-hat 4; Conservative
                                                                                                                      S DILEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1239
  US-09-801-784-22
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cassels, Frederick J.
JOORIS-Price, Lawrence
TITLE OF INVENTION: PEPTIDES FROM A CONCENSUS PEPTIDE OF
                                                                                                                                                                                                                                                                                                                                               Query Match 52.6%; Score 20; DB 9; Length 8; Best Local Similarity 80.0%; Pred. No. 5.4e+05; Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
CCMPUTER: IBM PC compatible
CCMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATERITE Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLI CS4-CFA/I FAMILY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NC
ANTI-SENSE: NC
ORIGINAL SOURCE:
ORGANISM: E. COII
STRAIN: CS4-CFA/I
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-801-784-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: CS4-CFA/I
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 37
CORRESSONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: P.O. BOX 2509
TELEPHONE: (703) 425-8405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-801-784-22
Sequence 22, Application US/09801764
Patent No. US200100.4668A1
GENERAL INFORMATION:
                TELEFAX: (702) 425-8436
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: E. coli
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STATE: VA
COUNTRY: US
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Sequence Sequence Seguence Seguence

Sequence 1189, Apple Sequence 2550, Apple Sequence 36, Appl Sequence 36, Appl Sequence 1189, Appl Sequence 15, Appl Sequence 15, Appl Sequence 25, Appl Sequence 20, Appl

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Sequence 20, Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Hung, Shi
TILLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Christopher
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Xia-Hua
APPLICANT: Sharp, Alan
APPLICANT: Grant, Anthony
A
US-08-747-599A-50
US-08-747-599A-51
US-08-912-954-140
US-08-912-954-140
US-09-187-859-1186
US-09-187-859-1186
US-09-187-859-1186
US-09-187-859-1189
US-09-183-26A-35
US-09-183-26A-36
US-09-183-56A-36
US-09-183-56A-36
US-09-183-56A-36
US-09-183-56A-36
US-09-183-56A-36
US-09-183-56A-36
US-09-183-56A-36
US-09-183-56A-36
US-09-183-542B-1189
US-09-183-542B-1189
US-08-08-650-639-115
US-08-08-650-639-115
US-08-144-4175-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 3; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRISSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 7
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Vismatches
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Patent No. 6093849
GENERAL INFORMATION:
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Rattus norvegicus
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Best Local Similarity 80.v
Best Local 4; Conservative
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US-C8-459-568-20
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                                                                                              October 20, 2003, 13:12:15 ; Search time 28 Seconds (without alignments) 13.600 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 72,
Sequence 78,
Sequence 72,
Sequence 72,
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Sequence 20,
Sequence 20,
Sequence 75,
Sequence 75,
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Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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Sequence ]
Sequence .
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Seguence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               5.1.6
Compugen Std.
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US-08-459-568-20
US-08-516-859A-20
US-08-516-859A-20
US-08-516-859A-35
US-08-516-859A-35
US-08-516-859A-35
US-08-528-706-75
US-08-528-706-75
US-08-528-706-75
US-08-528-706-75
US-08-528-706-75
US-08-528-706-75
US-08-518-71
US-08-518-71
US-08-518-71
US-08-518-71
US-08-518-71
US-09-528-706-72
US-09-528-706-73
US-09-528-706-73
US-09-528-706-73
                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                    328717 segs, 42310858 residues
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               GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
                                                                                                                                                           US-09-489-760A-1
38
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Match Length
                                                                        protein search,
                              Copyright
                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 9 Maximum DB seq length: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ........
                                                                                                                                                                                                                                                                                                                                                                        Post-processing:
                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ī
                                                                          CM protein
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                                                                                                                                                                                             Sequence:
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                                                                                                                                                                                         RESULT 4

US.-08-516-855A-20

Sequence 20, Application US/OBS16859A

Parent No. 6069201

Parent No. 6069201

Parent No. Hangy, Shi
APPLICANT HANGY, Shi
ITILE OF INVENTION: Zinc Finger Protein - Interacting
ITILE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 106

CORRESONDENCE STATE: ADDRESS:
ADDRESSEE: Campbell & Flores LLP

STREET: 4170 La Joha Willage Drive, Suite 700

CITY: San Diego
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblasioma Protein - Interacting
Zinc Finger Proteins
NITMER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6;
         Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURP. 92122
COMPUTER REACABLE FORM:
MEDINY TYPE: F'CUPPY disk
CCMPUTER: IBM PC comparible
OPERATING SYSTEM: PC_DOS/MS-DOS
SCFTWARE: Patentin PC_DOS/MS-DOS
SCFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/516,659A
FILING APPLICATION 54
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-NAX-1995
FILING DATE: 06-NAX-1995
FILING DATE: US-NAX-1995
ATCANEY/AGENT INPOSEATION: A
REGISTRATION NUMBER: 31,915
RESIDENCE/DOCKET NUMBER: 31,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 3; I
Pred. No. 2.5e+05;
    Score 21; DB 2;
Pred. No. 2.5e+05;
1; Mismatches 0
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US-05-586-472-20
US-05-586-472-20
Sequence 20, Application US/03586472
Patent No. 6323335
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.3%;
80.0%;
      55.3%;
80.0%;
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INFORMATION FOR SEQ ID NO: 2
    Guery Match
Best Local Similarity 80.0
Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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| EDLLE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLCGY:
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; Sequence 20 Application US/08399411
; Parent No. 5831008
; GENERAL INCRMATION:
    APPLICANT: Huang, Shi
    TITE OF INVENTION: Retinoblastoma Protein - Interacting
    TITE OF INVENTION: Zinc Finger Proteins
    NUMBER OF SEQUENCES: 93
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Campbell and Flores
    STREET: 4370 La Colla Village Drive, Suite 700
    CITY: San Diego
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21, DB 2, Length 6, Pred, No. 2.5e+05, 1, Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/59,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: DATA
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTOMEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LJ 1264
TELEFHCNE: (6:9) 535-9001
TELEFHCNE: (6:9) 535-9001
TELEFHCNE: (6:9) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SECURATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OVERTURE: TBM PC COMPATIBLE
OFFINARE: PATENTIN FOLOS/SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-901
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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amino acid
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TYPE: amino acid
TOPOLOGY: linear
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: EDLLE 5
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TOPOLCGY:
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GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Tank PC compatible
COMPUTER: PatentIN PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.3%; Score 21; DB 4; 80.0%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.3%; Score 21; DB 2;
80.0%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                  APPLICATION NUMBER: US 08/516,859
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGEY: INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECHMUNICATION INFORMATION:
TELEFDAX: (619) 535-8949
INFORMATION FOR SEC ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICE APPLICATION DATA:
APPLICATION WINEBER: US 08/399,411
ETLING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Sequence 75, Application US/08459568
; Patent No. 5811304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A. REGISTRAITCON NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P. TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (619) 535-900
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuery Match
Rost Local Similarity 80.00
Free 4; Conservative
                                                                                                                                                                                                                                                                                                                    SECUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 amine acids
                                                                                                                                                                                                                                                                                                                                              6 amino acids
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STATE: California
                                                                                                                                                                                                                                                                                                                                                            IYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                             US-09-528-706-20
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US-08-459-568-75
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APPLICANT: Huang, Sh:

TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Firger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.3%; Score 21; DB 4; Length 6; 80.0%; Pred. No. 2.5e+05; ative 1; Mismatches 0; Indels
                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-00S/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 32/09/586,472
FILING DATE: 01-000Mn-200
CLASSIFICATION: vUnknown>
PRIOR APPLICATION: vunknown>
                STREET: 4370 La Jolla Village Drive, Suite 700 CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Colla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,706
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATE: 17-MAR-2000
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
APPLICATION NUMBER: US 08/292,683
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SECUENCE DESCRIPTION: SEQ ID NO: 20:
ADDRESSEE: Campbell & Flores
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; Sequence 20, Application US/09528706
; Patent No. 6468985
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INFORMATION FOR SEQ ID NO: 20:
SEGUENCE CHARACTER: STICS:
LENGTH: 6 amino acids
                                                                                                                                      COMPUTER READABLE FORM:
                                                               STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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Best Local Similarity 80.0
Matches 4; Conservative
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15-09-586-472
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MEDIUW TYPE: FLORY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEITIN Release #1.0, Version #1.25
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CORRESPONDENCE ADDRESS:
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: CANTE CANTE CANTE
COMPUTER: ISM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.3%; Score 21; DB 3;
80.0%; Pred. No. 2.5e+05;
live 1; Mismatches 0
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APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-703-200
CLASSFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2003
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-MAR-1595
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTCHNEY/AGENT INFORMATION:
                                                                SOFTWARE: Patentin Release #1:0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-A405.995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
FILING DATE: 18-A405.1994
ATTOANEY/AGENT INFORMATION:
NAME: Campbell, Cattryn A.
RESIGNATION NUMBER: 1,815
RESIGNATION NUMBER: 1,815
RESIGNATION NUMBER: 1,815
REFERENCE/DOCKET NUMBER: 1,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 535-8949
INFORMATION FOR SEQ 10 NO: 7
SEQUENCE CHARRACTERISTICS:
LENGTH: 8 amino acids
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Sest Local Similarity 80.0
Matches 4, Conservative
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GY: linear
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Sequence 75, Application US/C8516859A
APPLICANT: Huang, Shi
TITLE OF INVENTION: Zinc Finger Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbedl & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
STRIET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATT: Huang, Sri
TITLE CF INVENTION: Zinc Finger Proteins
TITLE CF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ALDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.3%; Score 21; DB 2; Length 8; 80.0%; Pred. No. 2.5e+05; live 1; Mismatches 0; Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OFFMAINS: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 0.6-MAR.1955
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Carinyn A.
REGISTRATION NUMBER: 31,815
REFERRNCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF $35-9961
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARRATERISTICS:
LENGTH: 8 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               Sequence 75, Application US/08199411 Patent No. 5831008 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 4; Conservative
       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                               4 DDLLE 8
                                                                                                                                                       1 EDLLE 5
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US-08-399-411-75
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           Matches
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US-08-459-568-78
                                                            .S-08-459-568-72
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US-09-528-706-75
Sequence 75, Application US/09526706
Sequence 76, Application US/09526706
Sequence 76, Application US/09526706
SENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Zinc Finger Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
THREET: 4370 Lm Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.3%; Score 21; DB 4; Length 8; 80.0%; Pred. No. 2.5e+05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                             Score 21; DB 4; Length 8;
Pred. No. 2.5e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fateniin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,736
REFERENCE/DOCKET NUMBER: P-LC 4130
                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
FILING DATE:
RAPPLICATION NUMBER: US 08/292,683
FILING DATE:
APPLICATION NUMBER: US 08/292,683
FILING DATE:
APPLICATION NUMBER: US 08/292,683
ATONNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REPRENCE/DOCKET NUMBER: 9-LJ 1776
TELEPHONE: (6-9) 515-9001
TELEPHONE: (6-9) 515-9001
TELEPHONE: (6-9) 515-9001
TELEPHONE: GRANTICS: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     TCPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 75:
                TELECOMMUNICATION INFORMATION:
TELBEHONE: (619) 535-9001
TELBEACK: (619) 535-8049
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENTH: 8 amino acids
TYPE: amino acids
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Best Local Similarity Bulu
The Corservative
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Matches 4; Conservative
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CITY: San Diego
STATE: California
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TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.3%; Score 21; DB 2; Length 9; 80.0%; Pred. No. 2.5e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FEATURE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIOPPY disk
COMPUTER: PEOPPY disk
COMPUTER: PO-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 50
ATTORNEY/AGBNT INFORMATION:
NAME: Campbell Cathryn A.
RESTRATION NUMBER: 9-13
REFERENCE/DOCKET NUMBER: 9-13 1264
TELECOMMUNICATION INFORMATION:
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 2; ]
Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                         CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cartryth A.
REFERENCE/DOCKET NUMBER: 3:815
REFERENCE/DOCKET NUMBER: 9-LJ 1264
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 aming acids
SOFTWARE: Patentin Release #1.0, N
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
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Patent No. 5831008

GENERAL INFORMATION:
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4, Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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STREET: 4370 La Jol
CITY: San Diego
STATE: Callfornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                     Sequence 78, Application US/08399411
Parent No. 583108
| Parent No. 583108
| JERNEY PARTION: SALINGE Protein - Interacting ITLE OF INVENTION: Actinoblastoma Proteins | ITLE OF INVENTION: Zinc Finger Proteins | ITLE OF INVENTION: Zinc Finger Proteins | VINSEN ON ESQUENCES: 93 | CCRESSPONDENCE ADDRESS: ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.3%; Score 21; DB 2; Length 9; 80.0%; Pred. No. 2.5e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIPICATION: 530
ATTCRNEY/AGENT INFORMATION:
NAME: CAMPDELL, CATARYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DCCKET NUMBER: P-LJ 1264
TELECOXYUNICATION INFORMATION:
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TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 78
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0°
Matches 4; Conservative
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3Y: linear
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TOPOLOGY:
RESULT 15
US-08-399-411-78
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, Entered [jdelaval 20-Oct-03 11:06] SEQ1A vihddlleal

, Entered (jdelaval 20-Oct-03 11:07) SRQ1B vlrddlleal